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Fig. 1

NL1:

Diring .							`		•				!				700					
GGCT	CCT	CATO	TGC	AA	CAC	CTC	GGG	STC	AC	cccc	CGA	.CA	ACG	GT C	GTC	GGA	.GGG	AGA	.GC	GG	С	60
CTCC!	rcc	TCCC	TG	3TG	GGG	CCT	GT	CTG	GG'	TGAZ	AGC	cc	CTC	TGI	TCC	CCGA	.GGP	TCG	TC	CC	A	120
ACCC	CCA	GCCG	GG'	rgc	TCC	GAG	CCI	٩TG	GC	CGAC	CAC	CĀ	TCT	TC	GC2	AGCG	GGF	ATG	AT	CÄ	.G	180
								M	A	. D	T	:	ľ	F	G	· S	G	N	D	Q		12
TGGG	TTT	GCC	CA	ATG	ACC	GGC	AG	CTT	GC	CCT	rco	3AG	CCA	AG	CTG	CAG	ACGO	GC1	'GG	TC	:C	240
. W	v.	С	P	N	D	R	Q	L	P	į I	٠.	R	A	ĸ	L	Q	T	/G	W	5	3	32
GTGC	ACF	CCT	ACC	AGA	ACGG	AGA	\AG	CAG	AG	GAG	GAZ	٩GC	AGC	AC	CTC	AGC	CCG	3CG(3AC	GI	Ġ	300
v .	н	T	Υ.	Q	T	E	ĸ	Q	· F	R F	R	ĸ	Q	Н	L	s	P	A	E	•	V	. 52
GAGG	CC2	YTCC	TGC	AG	GTC <i>I</i>	ATC	CAG	AGC	GC	CAGA	GC	GG	CTCC	BAC	GTC	CTG	GAG	CAG	CAC	3A(SA ·	360
E	A	I	L	Q	V	I	Q	R	. 1	A. 1	E	R	L	D	v	L	E	Q	Q	: :	R	72
ATC	GGG	CGGC	TGG	TG	GAG	cec	CTG	GAG	3AC	CCAT	GA	GG	CGGZ	TA	GTG	ATG	GGG	AAC	GG	ÇC'	rg	420
I	G	R	L	٧	E	R	L	E		T I	M	R	Ŗ	N	V	M	G	N	· G	;	L.	92`
TCC	CAG	TGTC	TG	стс	TGC	GGG	GAG	€GT(GC'	TGGG	CT	TC	CTG	GGC	AGC	CTCG	TCG	GTG	TT	ĊT	GC	430
s	Q	c	L	L	С	G	E	V	7	L	G	F	L	G	s	S	s	V	E	?	Ċ	112
AAA	GAC	TGCF	\GG/	AAG	GTC	TGG	AA	GAG	GT	CGGC	3 G G	CC	TGG	TTC	CTAC	CAAA	GGG	CTC	cc	CA	AG	540
к	D	c.	R	κ	٧	W	κ	F	₹.	s	G	A	W	F	Y	K	G	L	.]	5	ĸ	132
TAT	ATC	TTG	ccc	сте	AAG	ACC	ccc'	TGG	CC	GAG	CTO	FAT	'GAG	CC	CA	GTT	CCG	ACCI	TG	GC	cc	600
Y	I	L	P	L	ĸ	T	P	(G	R	A	D	E	E	Q	E	R	. E	? 1	M	P	152
ACG	GA	ACCG	GCA	GA(GCG/	AGAC	3CC	CAG	ΑA	GCT	CT	GAG	ACC	AG	CCG	CAT	CTA	CAC	GT (GG	GCC	660
T	E	P	A	E	R	E	P	•	R	s	s	E	T	5	S P	1	(Y	·, •	•	W	Α	172
CGP	AGG	A AGA	GTC	GT'	rtco	CAG'	ľGA	CAC	TC	GACA	GT	GA	CTCC	GA	тст	TAG	CTC	CTC	CAC	GC	ста	720
R	G	R	V	·V	s	. s)	s	Œ	s	D	s	.]	D I	. :	s s	3 3	S	s	L	192
GAC	GA.	CAGA	CTC	CC	ATC	CAC'	TGG	GG'	rc <i>i</i>	AGGG	AC	CG	GAA	A GG	CGP	CAA	ACC	CTG	GA)	٩G	GAG	780
E	: [R	L	F	s	т		3	v	R	D	R	ĸ	. (G I	o :	K I	?	W	ĸ	E	212
TC	AGG	TGGC	AG	CGT	GGA	GGC	cco	CA	GG	ATGO	GG	TT	CAC	CCP	ACC	ccśc	GGG	CCA	CC	TC	ттт	840
	3 6	3 G	s	; v	, E	I	A 1	P	Ŕ	М	G	E	т		Q	P	A (3	Н	L	· F	232

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	GGGTTGCAGAGCAGCCTGGCCAGTGGTGAGACGGGCACAGGCTCTGCTGACCCGCCAGGG	900 [.]
	G L Q S S L A S G E T G T G S A D P P G	252
	GGAGGGACAGGCTCTGCTGACCCGCCAGGGGGACCCCGCCCCGGGCTGACCCGAAGGGCC	960
,	G G T G S A D P P G G P R P G L T R R A	272
	CCGGTAAAAGACACCTGGACGAGCCCCCGCTGCTGACGCAGCTCCAGCAGGCCCCTCC	1020
	PVK DTP GRAPAAD AA PA GPS	292
	AGCTGCCTGGGCTGAGGTGTCTGGTGCCTGGAACAGACTTCCCTGTGGAGGATTCCTGCC	1080
	SCLG*	296
	AGACCCTGCCCGGCTCCTCGCCGGTCCTTGTGCCCTCACCAGACACCCTGTTGGCC	1140
,	ATGACTCAACAAACCAGTGTTGGGAGCCGTCTGCCTCCCCAGCTCAGTGCCTTTCTGCAC	1200
:	CCCTTCTCTCCTGGGGAGCTGTCTGCATCCGCCACCCCCTCCAACCACTGCCCTCAGCCC	1260
i	CCGACCTTATTTATTACCCTCCCCCCCCCCCCCCCCCCC	1320
	TTTGCGCGTGTCTTGGGTTGGGCTGGGGGGTTTCCCACATGCAGTGTCAGAGGGGCCGCC	1380
	CGGTGGGGCTATCTCCGTTGCTATATTAATGGCAAGACTAAATGAAACCTAGGGCACGGC	1440
	CTCCGAAGCTGCGTGTGGCCCCTTAGAGGTGAGCATCAGAGCCAGAGCAGTGAGGGGGAG	1500
	ACTCACCCACCTCTCCCTTCCCTTCAGCTCTGGGAGGCAGGC	1560
	ATGGGCTGGCCCAGGACCGCGGTGAAACCTGGGTCTGTTTAGTTTCTTTGGTTTTTGTA	1620
	TGTTTGTTTGTTTTTGACACAGTCTCGCTTTGTTGCCCAGGCTGGGGTGCAGTGGCACGA	1680
	TCGCGGCTCACTGCAACCTCCACCTCCCGGGCTCAAGCGATTCTCTCACCTCAGCCTCCT	1740
	GAGTAGGTGGGATTACAGATGCCCGCCACCCACACCCAGTTAATTTTTGTATTTTTAGAAG	1800
	AGATGGGGTTTCTCCATGTTGGCCAGGCTGGTCTTGAACTCCTGGTCTCAAGTGATCCGC	1860
	CCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGCACCCAATCCTATT	1920
	AGGTTTCTTTGAATCCCCTCATGGCCTGCCTGGTTTTTGCTCAGCCTGTCTTCAGCTTGA	1980
	GGAGCTGGGAAGCTCTGGTGGATGCTATGAACTCACTTGCTGAAGAGCAGCGTTCAGGTG	2040
	CATCCCCAGCCAGGGCACGTGGCTCCCTCAGCCATGAATTCACTTCTCTTCAGGAGGTTT	2100
. !	GGCTTGGCATGAAAATACTTCATTCAGAGTATGGGCAAATGCTTCTGGAAAAACCCTTCCC	2160
·	TGAAGAGAGAACGTGTGTGTGTGTGTCGGTGATCACACCCTCCCATCCTTCCT	2220
- 1	CTGCCCCAAACCCCGGGTTCCTGGGTCTGGAAGGGCCTTCTCTCCAAGCTGGGAGCTCCT	2280
	GGGCCCCACCATTCACTTTTTGTCCTTGCTGCCAAACAGTAAAGAAACTCACTTTC	2340
	CCTGTGGCACGTTATGCTTCAGAATTAAAACAATGAAGATTAAAA	2385

Fig. 2

CL1:

GGC'	rcc'	TCA	TCT	GGA	ACA	CCT	CGG	GTC	ACC	ccc	GAC	AAC	GGT	GGT	GGG	AGG	GAG	AGC	GGC	60
CTC	CTC	CTC	CCT	GGT	GGG	GCC'	TGT	CTG	GGI	'GA,	\GCC	CCT	CTG'	ттс	CCG	AGG	ATC	GTC	CCA	120
ACC	ccc	AGC	CGG	GTG	CTC	CGA	GCC	ATG	GCC	CGAC	CACC	ATC	TTC	GGC	AGC	GGG	AAT	gat	CAG	180
		2					•	M	A.	D	T	I	F	G	s	G	'n	D	Q.	12
TGG	ЭТТ	TGC	ccc.	ААТ	GAC	CGG	CAG	СТТ	GCC	CTI	CGA	GCC	AAG	CTG	CAG	ACG	GGC'	TGG	TCC	240
W	v	С	P	N	D	R	Q	L	A	L	R	A	ĸ	L	Q	T	G	W	s	32
GTG	CAC	ACC	TAC	CAG	ACG	GAG	AAG	CAG	AGG	AGG	AAG	CAG	CAÇ	CTC	AGC	CCG	GCG	GAG	GTG	300
۷	Н	T	Y	Q	T	E	ĸ	Q	R	R	ĸ	Q	н	L	s	P	Α	Έ	V.	52
GAG	GCC.	ATC	CTG	ĊAG	GTC	ATC	CAG	AGG	GCA	\GAG	CGG	CTC	GAC	GTC	CTG	GAG	CAG	CAG	AGA	360
E	A	I	Ĺ	Q	v	I	Q	R	A	E	R	L	D.	v	L	E	Q.	Q	R	, 72
ATC	GGG	CGG	CTG	GTG	GAG	CGG	CTG	GAG	ACC	CATO	AGG	CGG	AAT	GTG	ATG	GGG	AAC	GGC	CTG .	420
I	G	R.	L.	v	E	R	L	E	T	М	R.	R	N	v	М	G	N	G	L	92
TCC	CAG	TGT	CTG	CTC	TGC	:GGG	GAG	GTG	сте	GGG	ттс	CTG	GGC	AGC	TCG	TCG	GTG'	TTC	TGC	480
s	Q	C	L	Ĺ	С	G	E	v	Ļ	G	. F	L	G	s	s	s	. A .	F	С	112
AAA	GAC	TGC	AGG	AAG	AAA	GTC	TGC	ACC	:AA	atg1	rggg	ATC	GAG	GCC	TCC	CCT	GGC	CAG	AAG	540
к	D	C ·	Ŕ	ĸ	к	v	С	т	ĸ	C	G	I	E	Α	s	P	G	Q	к	132
CGG	ccċ	CTG	TGG	CTG	TGT	'AAG	ATC	TGC	AGI	rgac	CAÁ	AGA	GAG	GTC	TGG	AAG	AGG	TCG	GGG	600
R	P	L	W	L	С	к	. I	C	s	E	Q	R	E	V.	W	к	R	s	G	152
GCC'	TGG	TTC	TAC	AAA	.GGG	CTC	ccc	AAG	TAT	TAT	TTG	CCC	CTG.	A AG	ACC	CCI	'GGC	CGA	GCT	660
A	W.	F	Y	к	G	L	P	K	Y	I	L	P	L	ĸ	P	P	G	R	A	172
GAT	GAC	ccc	CAC	TTC	CGA	CCT	TTG	ccc	ACC	GA/	ACCG	GCA	GAG	CGA	GAG	ccc	AGA	AGC	TCT	720
D	D	P	н	F	R	P	· L	P	Ŧ	E	P	A	E	R	E	P	R	s	s	192
GAG	ACC	AGC	CGC	 АТС	ጥልር	ACG	ጥርር	GCC	ירפו	rco.	A A G B	ርሞር	C TOTAL	ምርር	• В С-П	CAC	ነ <u>ነ</u> ርመ	CNO	አ ርሞ	780
E.	T	s	R		Y	т	W			: '										
		,									R				S	D		D 	.s	212
GAC?					•												:			840
ď	s	D	L	S	s	S	S	L	E	D	R	L	P	s	T	G	V	R	D	232

CGGAAAGGCGACAAACCCTGGAAGGAGTCAGGTGGCAGCGTGGAGGCCCCCAGGATGGGG 900 RKGD KP W K E S G G S V E A P R M G 252 TTCACCCAACCCGCGGGCCACCTCTTTGGGTTGCAGAGCAGCCTGGCCAGTGGTGAGACG 960 FTQPAGHL FGL QS SLA S G E T 1020 GGCACAGGCTCTGCTGACCCGCCAGGGGGAGGGACAGGCTCTGCTGACCCGCCAGGGGGA G T G S A D P P G G G T G S A D P P G G 292 CCCCGCCCGGGCTGACCCGAAGGGCCCCGGTAAAAGACACACCTGGACGAGCCCCCGCT 1080 312 PRPGLT RRAPV KD TPG RAPA GCTGACGCAGCTCCAGCAGCCCCTCCAGCTGCCTGGGCTGAGGTGTCTGGTGCCTGGAA 1140 325 ADAA PA G P S S C L G CAGACTTCCCTGTGGAGGATTCCTGCCAGACCCTGCCCGGCTCCTCCCTGACCGGTCCTT 1200 GTGCCCTCACCAGACACCCTGTTGGCCATGACTCAACAAACCAGTGTTGGGAGCCGTCTG 1260 CCTCCCCAGCTCAGTGCCTTTCTGCACCCCTTCTCTCTGGGGAGCTGTCTGCATCCGCC 1320 CCCAATCTACCTGGTGATGATTTTAAGTTTGCGCGTGTCTTGGGTTGGGCTGGGGGGGTTT 1440 CCCACATGCAGTGTCAGAGGGGCCGCCCGGTGGGGCTATCTCCGTTGCTATATTAATGGC 1500 AAGACTAAATGAAACCTAGGGCACGGCCTCCGAAGCTGCGTGTGGCCCCTTAGAGGTGAG 1560 CATCAGAGCCAGAGCAGTGAGGGGGAGACTCACCCACCCTCTCCCTTCCCTTCAGCTCT 1620 GGGAGGCAGGCGCAGTGCCCCCTCCCATGGGCTGGCCCAGGACCGCGGGTGAAACCTGG 1680 TGCCCAGGCTGGGGTGCAGTGGCACGATCGCGGCTCACTGCAACCTCCACCTCCCGGGCT 1800 CAAGCGATTCTCTCACCTCAGCCTCCTGAGTAGGTGGGGATTACAGATGCCCGCCACCACA 1860 CCCAGTTAATTTTTGTATTTTTAGAAGAGATGGGGTTTCTCCATGTTGGCCAGGCTGGTC 1920 TTGAACTCCTGGTCTCAAGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAG 1980

GTGTGAGCCACCGCACCCAATCCTATTAGGTTTCTTTGAATCCCCTCATGGCCTGCCT	2040
TTTTTGCTCAGCCTGTCTTCAGCTTGAGGAGCTGGGAAGCTCTGGTGGATGCTATGAACT	2100
CACTTGCTGAAGAGCAGCGTTCAGGTGCATCCCCAGCCAG	2160
ATGAATTCACTTCTCTCAGGAGGTTTGGCTTGGCATGAAAATACTTCATTCA	2220
GGCAAATGCTTCTGGAAAACCCTTCCCTGAAGAGAGAACGTGTGTGT	2280
ATCACACCCTCCCATCCTTCCTGCCTCCTGCCCAAACCCCGGGTTCCTGGGTCTGGAAG	2340
GGCCTTCTCCCAAGCTGGGAGCTCCTGGGCCCCCACCATTCACTTTTTGTCCTTGCTGC	2400
TGGCAAACAGTAAAGAAACTCACTTTCCCTGTGGCACGTTATGCTTCAGAATTAAAACAA	2460
TGAAGATTAAAA	2472

Fig. 3

CL2: 60 CTCCTCCTCCTGGTGGGGCCTGTCTGGGTGAAGCCCCTCTGTTCCCGAGGATCGTCCCA 120 ACCCCAGCCGGGTGCTCCGAGCCATGGCCGACACCATCTTCGGCAGCGGGAATGATCAG 180 GAACAGGACCAACACAGTCCCTGGTCTTAAAGCACAGGTGGGCAGAGGCTGCAGACGGGC 300 TGGTCGGTGCACACCTACCAGACGGAGAAGCAGGAGGAAGCAGCACCTCAGCCCGGCG 360 GAGGTGGAGGCCATCCTGCAGGTCATCCAGAGGGCAGAGCGGCTCGACGTCCTGGAGCAG 420 CAGAGAATCGGGCGGCTGGTGGAGCCGCTGGAGACCATGAGGCGGAATGTGATGGGGAAC 480 R R N V M G N GGCCTGTCCCAGTGTCTGCTCTGCGGGAGGTGCTGGGCTTCCTGGGCAGCTCGTCGGTG 540 LSQCLLC GEV LG FLG SS 28 TTCTGCAAAGACTGCAGGAAGAAAGTCTGCACCAAATGTGGGATCGAGGCCTCCCCTGGC 600 F C K D C R K K V C T K C G I E A S P G 48 CAGAAGCGGCCCCTGTGGCTGTGAAGATCTGCAGTGAGCAAAGAGAGGTCTGGAAGAGG 660 Q K R P L W L C K I C S E Q R E V W K R 68 TCGGGGGCCTGGTTCTACAAAGGGCTCCCCAAGTATATCTTGCCCCTGAAGACCCCTGGC 720 S G A W F Y K G L P K Y I L P L K T 88 CGAGCTGATGACCCCCACTTCCGACCTTTGCCCACGGAACCGGCAGAGCGAGAGCCCAGA 780 R A D D P H F R P L P T E P A E R E P R 108 AGCTCTGAGACCAGCCGCATCTACACGTGGGCCCGAGGAAGAGTGGTTTCCAGTGACAGT 840 128 R G R V V SSETSRIY T W A GACAGTGACTCGGATCTTAGCTCCTCCAGCCTAGAGGACAGACTCCCATCCACTGGGGTC 900 148 E D S. S. L. s s AGGGACCGGAAAGGCGACAAACCCTGGAAGGAGTCAGGTGGCAGCGTGGAGGCCCCCAGG 960 168 G D K P W K E S G G S V E A D R K

ATGGGGTTCACCCAACCCGCGGGCCACCTCTTTGGGTTGCAGAGCAGCCTGGCCAGTGGT 1020 M G F T Q P A G H L F G L Q S S L A E TGT GS AD PPG GG TGS AD PP GGGGGACCCCGCCCCGGGCTGACCCGAAGGGCCCCGGTAAAAGACACACCTGGACGAGCC 1140 GPR PG LT RRA PV KDT PG RA CCCGCTGCTGACGCAGCTCCAGCAGGCCCCTCCAGCTGCCTGGGCTGAGGTGTCTGGTGC 1200 AADAA PAGPS SC LG * CTGGAACAGACTTCCCTGTGGAGGATTCCTGCCAGACCCTGCCCGGCTCCTCCCTGACCG 1260 GTCCTTGTGCCCTCACCAGACACCCTGTTGGCCATGACTCAACAAACCAGTGTTGGGAGC 1320 CGTCTGCCTCCCCAGCTCAGTGCCTTTCTGCACCCCTTCTCTCTGGGGAGCTGTCTGCA 1380 CACACCCCAATCTACCTGGTGATGATTTTAAGTTTGCGCGTGTCTTGGGTTGGGCTGGG 1500. GGGTTTCCCACATGCAGTGTCAGAGGGGCCGCCCGGTGGGGCTATCTCCGTTGCTATATT 1560 AATGGCAAGACTAAATGAAACCTAGGGCACGGCCTCCGAAGCTGCGTGTGGCCCCTTAGA 1620 AGCTCTGGGAGGCAGGCGCAGTGCCCCCCTCCCATGGGCTGGCCCAGGACCGCGGGTGAA 1740 ACCTGGGTCTGTTTAGTTTCTTTGGTTTTGTATGTTTTGTTTTGACACAGTCTCG 1800 CTTTGTTGCCCAGGCTGGGGTGCAGTGGCACGATCGCGGCTCACTGCAACCTCCACCTCC 1860 CGGGCTCAAGCGATTCTCTCACCTCAGCCTCCTGAGTAGGTGGGATTACAGATGCCCGCC 1920 ACCACACCCAGTTAATTTTTGTATTTTTAGAAGAGATGGGGTTTCTCCATGTTGGCCAGG 1980 CTGGTCTTGAACTCCTGGTCTCAAGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGA 2040 TTACAGGTGTGAGCCACCCCAATCCTATTAGGTTTCTTTGAATCCCCTCATGGCCT 2100 GCCTGGTTTTTGCTCAGCCTGTCTTCAGCTTGAGGAGCTGGGAAGCTCTGGTGGATGCTA 2160

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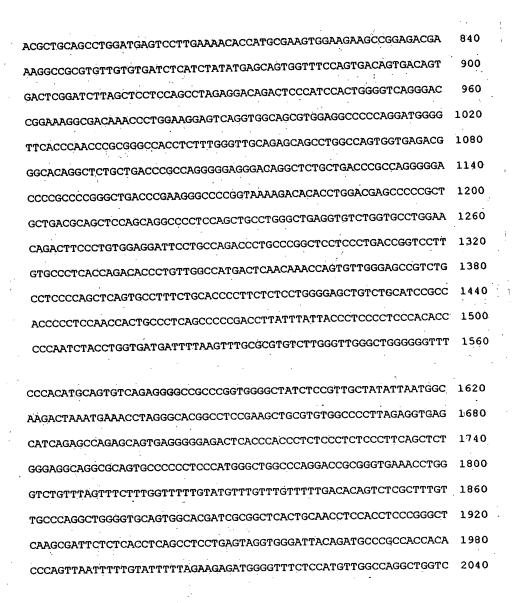
TCAGCCATGAATTCACTTCT	こうしゅうしゅう スペート・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・	ጥርርር ርጥጥርርር CA	ጥ ር ል ል ል ጥ ል ር ጥ	тсаттсас	2280
AGTATGGGCAAATGCTTCTG		•			2340
TCGGTGATCACACCCTCCCA	TCCTTCCTGCCT	CCTGCCCCAA	ACCCCGGGTT	CCTGGGTC	2400
TGGAAGGCCTTCTCCAA	GCTGGGAGCTCC	TGGGCCCCA	CCATTCACTT	TTTGTCCT	2460
TGCTGCTGGCAAACAGTAAA	GAAACTCACTTT	CCCTGTGGCA	CGTTATGCTT	CAGAATTA	2520
AAACAATGAAGATTAAAA		•	:		25.3.8
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Fig. 4

CL3:

GGCTCCTCATCTGGAACACCTCGGGTCACCCCCGACAACGGTGGTGGGAGGGA	
CTCCTCCTCCTGGTGGGGCCTGTCTGGGTGAAGCCCCTCTGTTCCCGAGGATCGTCCCA 120	
ACCCCCAGCCGGGTGCTCCGAGCCATGGCCGACACCATCTTCGGCAGCGGGAATGATCAG 180	
M ADT IFGS GNDQ 12	
TGGGTTTGCCCCAATGACCGGCAGCTTGCCCTTCGAGCCAAGCTGCAGACGGGCTGGTCC 240	
WVCPNDRQLALRAKLQTGWS 32	
GTGCACACCTACCAGACGGAGAAGCAGAGGAGGAAGCACCTCAGCCCGGCGGAGGTG 300	•
VHTYQTEKQRRKQHLSPAEV 52	
GAGGCCATCCTGCAGGTCATCCAGAGGGCAGAGCGGCTCGACGTCCTGGAGCAGCAGAGA 360	
EAILQVIQ RAER L DVL EQ QR 72	
ATCGGGCGGCTGGAGCCGGCTGGAGACCATGAGGCGGAATGTGATGGGCAATGTGATGGGCGGAATGTGATGGGCGGAATGTGATGGAGGCGGAATGTGATGGAGGCGGAATGTGATGGAGGCGGAATGTGATGGAGGCGGAATGTGATGGAGGCGGAATGTGATGGAGGCGGAATGTGATGGAGGCGGAATGTGATGGAGGCGGAATGTGATGGAGGCGGAATGTGATGGAGGCGGAATGTGATGATGATGATGATGATGATGATGATGATGAT	
IGRL VERLETMR R NVM GN GL 92	
TCCCAGTGTCTGCTCTGCGGGAGGTGCTGGGCTTCCTGGGCAGCTCGTCGGTGTTCTGC 480	
SQCLLCGEVLGFLGSSSV FC 112	
AAAGACTGCAGGAAGAAAGTCTGCACCAAATGTGGGATCGAGGCCTCCCCTGGCCAGAAG 540	ı
K D C R K K V C T K C G I E A S P G Q K 132	; ;
CGGCCCTGTGGCTGTAAGATCTGCAGTGAGCAAAGAGAGGTCTGGAAGAGGTCGGGG 600)
RPLWLCKICSEQREVWKRSG 152	?
	ċ
GCCTGGTTCTACAAAGGGCTCCCCAAGTATATCTTGCCCCTGAAGACCCCTGGCCGAGCT 660	3
AWFYKGLPKYILPLKII	
GATGACCCCCACTTCCGACCTTTGCCCACGGAACCGGCAGAGCGAGAGCCCAGAAGCTCT 72	0
D D P H F R P L P T E P A E R E P R S S 19	2
GAGACCAGCCGCATCTACACGTGGGCCCGAGGAAGAGTCGTAGGAAGAAGTGCTGATCC 78	0
TO THE ARGRY VGRKC * 21	Ċ



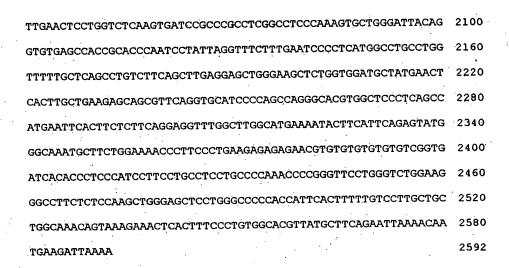


Fig. 5

CL4:

GGCTCCTCATCTGGAACACCTCGGGTCACCCCCGACAACGGTGGTGGGAGGGA	60
$\tt CTCCTCCTCCTGGTGGGGCCTGTCTGGGTGAAGCCCCTCTGTTCCCGAGGATCGTCCCA$	120
ACCCCAGCCGGGTGCTCCGAGCCATGGCCGACACCATCTTCGGCAGCGGGAATGATCAG	180
TGGGTTTGCCCCAATGACCGGCAGCTTGCCCTTCGAGCCAAGCACTGACTG	240
GAACAGGACCAACACAGTCCCTGGTCTTAAAGCACAGGTGGGCAGAGGCTGCAGACGGGC	300
TGGTCCGTGCACACCTACCAGACGGAGAAGCAGAGGAGGAAGCAGCACCTCAGCCCGGCG	360
GAGGTGGAGGCCATCCTGCAGGTCATCCAGAGGGCAGAGCGGCTCGACGTCCTGGAGCAG	420
CAGAGAATCGGGCGGCTGGAGCGGCTGGAGACCATGAGGCGGAATGTGATGGGGAAC	480
M R R N V M G N	8
GGCCTGTCCCAGTGTCTGCTCTGCGGGGAGGTGCTGGGCTTCCTGGGCAGCTCGTCGGTG	540
G L S Q C L L C G E V L G F L G S S S V	2,8
TTCTGCAAAGACTGCAGGAAGAAAGTCTGCACCAAATGTGGGATCGAGGCCTCCCCTGGC	600
F C K D C R K K V C T K C G I E A S P G	4.8
CAGAAGCGGCCCCTGTGGCTGTAAGATCTGCAGTGAGCAAAGAGAGGTCTGGAAGAGG	660
Q K R P L W L C K I C S E Q R E V W K R	68
TCGGGGGCCTGGTTCTACAAAGGGCTCCCCAAGTATATCTTGCCCCTGAAGACCCCTGGC	720
S G A W F Y K G L P K Y I L P L K T P G	88
CGAGCTGATGACCCCCACTTCCGACCTTTGCCCACGGAACCGGCAGAGCGAGAGCCCAGA	780
RADDPHFRPLPTEPAEREPR	108
AGCTCTGAGACCAGCCGCATCTACACGTGGGCCCGAGGAAGAGTCGTAGGAAGAAAGTGC	840
S S E T S R I Y T W A R G R V V G R K C	128
TGATCCACGCTGCAGCCTGGATGAGTCCTTGAAAACACCATGCGAAGTGGAAGAAGCCGG	900
AGACGAAAGGCCGCGTGTTGTGTGATCTCATCTATATGAGCAGTGGTTTCCAGTGACAGT	` 960
GACAGTGACTCGGATCTTAGCTCCTCCAGCCTAGAGGACAGACTCCCATCCACTGGGGTC	1020
AGGGACCGGAAAGGCGACAAACCCTGGAAGGAGTCAGGTGGCAGCGTGGAGGCCCCCAGG	1080
A THE COORTING A CECCA A CECCACACACACACTETTTGGGTTTGCAGAGCAGCCTGGCCAGTGGT	1140

GAGACGGGCACAGGCTCTGCTGACCCGCCAGGGGGGGGACAGGCTCTGCTGACCCGCCA 1200 GGGGGACCCCGCCCGGGCTGACCCGAAGGGCCCCGGTAAAAGACACACCTGGACGAGGC 1260 CCCGCTGCTGACGCAGCTCCAGCAGGCCCCTCCAGCTGCCTGGGCTGAGGTGTCTGGTGC 1320 CTGGAACAGACTTCCCTGTGGAGGATTCCTGCCAGACCCTGCCCGGCTCCTCCCTGACCG 1380 GTCCTTGTGCCCTCACCAGACACCCTGTTGGCCATGACTCAACAAACCAGTGTTGGGAGC 1440 CGTCTGCCTCCCCAGCTCAGTGCCTTTCTGCACCCCTTCTCTCCTGGGGAGCTGTCTGCA 1500 CACACCCCAATCTACCTGGTGATGATTTTAAGTTTGCGCGTGTCTTGGGTTGGGCTGGG 1620 GGGTTTCCCACATGCAGTGTCAGAGGGGCCGCCCGGTGGGGCTATCTCCGTTGCTATATT 1680 AATGGCAAGACTAAATGAAACCTAGGGCACGGCCTCCGAAGCTGCGTGTGGCCCCTTAGA 1740 AGCTCTGGGAGGCAGGCGCAGTGCCCCCTCCCATGGGCTGGCCCAGGACCGCGGGTGAA 1860 ACCTGGGTCTGTTTAGTTTCTTTGGTTTTTGTATGTTTTGTTTTTTTGACACAGTCTCG 1920 CTTTGTTGCCCAGGCTGGGGTGCAGTGGCACGATCGCGGCTCACTGCAACCTCCACCTCC 1980 CGGGCTCAAGCGATTCTCTCACCTCAGCCTCCTGAGTAGGTGGGATTACAGATGCCCGCC 2040 ACCACACCAGTTAATTTTTGTATTTTTAGAAGAGATGGGGTTTCTCCATGTTGGCCAGG 2100 CTGGTCTTGAACTCCTGGTCTCAAGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGA 2160 TTACAGGTGTGAGCCACCGCACCCAATCCTATTAGGTTTCTTTGAATCCCCTCATGGCCT 2220 GCCTGGTTTTTGCTCAGCCTGTCTTCAGCTTGAGGAGCTGGGAAGCTCTGGTGGATGCTA 2280 TCGGTGATCACACCCTCCCATCCTTCCTGCCTCCTGCCCCAAACCCCGGGTTCCTGGGTC 2520 TGGAAGGGCCTTCTCCCAAGCTGGGAGCTCCTGGGCCCCCACCATTCACTTTTTGTCCT 2580 TGCTGCTGGCAAACAGTAAAGAAACTCACTTTCCCTGTGGCACGTTATGCTTCAGAATTA 2640 2658 AAACAATGAAGATTAAAA

1
rgga acaccicgggicacc cccgacaacggiggi
3 LC1 GGCTCCTCATCTGGA ACACCTCGGGTCACC
ACACCTCGGGTCACC CCCGACAACGGTGGT GGGAGGGAGAGCGGC CTCCTCCTCCTGGT GGGGCCTGTCTGGGT
6 LC4 GGCTCCTCATCTGGA ACACCTCGGGTCACC CCCGACAACGGTGGT GGGAGGGGAG
120 121
TCCCA ACCCCAGCCGGGIG CICCGAGCCAIGGCC GACACCAICITCGGC AGCGGGAAIGAICAG
CCGAGGATCGTCCCA ACCCCAGCCGGGTG CTCCGAGCCATGGCC GACACCATCTTCGGC AGCGGGAATGATCAG
CCGAGGAICGICCCA ACCCCCAGCCGGGIG CICCGAGCCAIGGCC GACACCAICTICGGC AGCGGGAAIGAICAG
CCGAGGATCGTCCCA ACCCCCAGCCGGGTG
CCGAGGATCGTCCCA ACCCCGAGCCGGGTG
GIIC CCGAGGAICGICCCA ACCCCCAGCCGGGIG CICCGAGCCAIGGCC GACACCAICTICGGC

	181 195	196	210 211 22	225 226 240	241	255 256 270	0
1 NOC	1 NOC2 TGGGTTTGCCCCAAT	CCCAAI GACCGGCAGCTIGCC CTTCGAGCCAAGC	: CTTCGAGCCAAGC				108
2 NL1	2 NL1 TGGGTTTGCCCCAAT GACCGGCAGCTTGCC CTTCGAGCCAAGC	GACCGGCAGCTTGCC	CTTCGAGCCAAGC		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		223
3 LC1	3 LC1 TGGGTTTGCCCCAAT GACCGGCAGCTTGCC CTTCGAGCCAAGC-	GACCGGCAGCTTGCC	CTTCGAGCCAAGC				223
4 LC2	4 LC2 TGGGTTTGCCCCAAT GACCGGCAGCTTGCC CTTCGAGCCAAGCAC	GACCGGCAGCTTGCC	CTTCGAGCCAAGCAC	TGACTGCACAGCAGT	GAACAGGACCAACAC	TGACTGCACAGCAGT GAACAGGACCAACAC AGTCCCTGGTCTTAA	270
5 LC3	5 LC3 TGGGTTTGCCCCAAT GACGGCAGCTTGCC CTTCGAGCCAAGC	GACCGGCAGCTTGCC	CTTCGAGCCAAGC		1		223
6 LC4	6 LC4 TGGGTTTGCCCCAAT GACCGGCAGCTTGCC CTTCGAGCCAAGCAC TGACTGCACAGTAGT GAACAGGACCAACAC AGTCCCTGGTCTTAA	GACCGGCAGCTTGCC	CTTCGAGCCAAGCAC	TGACTGCACAGCAGT	SAACAGGACCAACAC	AGTCCCTGGTCTTAA	270
	271 285	286	300 301 315	315 316 330 331	331 345	5 346 360	
1 NOC2	1	TGCAGACGGGC	TGGTCCGTGCACACC	TGCAGACGGGC TGGTCCGTGCACACC TACCAGACGGAGAAG CAGAGGAGGAAGCAG CACCTCAGCCGGCG	CAGAGGAGGAAGCAG	CACCTCAGCCCGGCG	179
2 NL1		TGCAGACGGGC	TGGTCCGTGCACACC	-TGCAGACGGGC TGGTCCGTGCACACC TACCAGACGAGAAG CAGAGGAGGAAGCAG CACCTCAGCCGGGCG	сяваввавваявсяв	CACCTCAGCCCGGCG	294
3 LC1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TGCAGACGGGC	TGGTCCGTGCACACC	TGCAGACGGGC TGGTCCGTGCACACC TACCAGACGGAGAAG CAGAGGAAGGAAGCAG CACCTCAGCCGGCG	сядававаявсяв	CACCTCAGCCCGGCG	294
4 LC2	4 LC2 AGCACAGGTGGGCAG	AGGCTGCAGACGGGC	TGGTCGGTGCACACC	AGGCTGCAGACGGGC TGGTCGGTGCACACC TACCAGACGAAGAAG CAGAGGAAGGAAGCAG CACCTCAGCCGGCG	CAGAGGAAGCAG	CACCTCAGCCCGGCG	360
5 LC3		TGCAGACGGGC	TGGTCCGTGCACACC	TGCAGACGGGC TGGTCCGTGCACACC TACCAGACGGAGAAG CAGAGGAGGAAGCAG CACCTCAGCCCGGCG	CAGAGGAGGAAGCAG	CACCTCAGCCCGGCG	294
6 . LC4	6 LC4 AGCACAGGTGGGCAG AGGCTGCAGACGGGC TGGTCCGTGCACACC TACCAGACGGAGAAG CAGAGGAAGCAG CACCTCAGCCCGGCG	AGGCTGCAGACGGGC	TGGTCCGTGCACACC	TACCAGACGGAGAAG	CAGAGGAGGAAGCAG	CACCTCAGCCCGGCG	360
٠.	361 375	375 376 390	390 391 405	405 406 420	420 421 435	5 436 450	
1 NOC2	1 NOC2 GAGGIGGAGGCCAIC CIGCAGGICAICCAG AGGGCAGAGCGGCIC GACGICCIGGAGCAG CAGAGAAICGGGGGG CIGGIGGAGCGGCIG	CTGCAGGTCATCCAG	AGGCAGAGCGGCTC	GACGTCCTGGAGCAG	CAGAGAATCGGGCGG	CTGGTGGAGCGGCTG	269
2 NLI	2 NLI GAGGTGGAGGCCATC CTGCAGGTCATCCAG AGGGCAGAGCGGCTC GACGTCCTGGAGCAG CAGAGAATCGGGGCGG CTGGTGGAGCGGCTG	CTGCAGGTCATCCAG	AGGCCAGAGCGGCTC	GACGTCCTGGAGCAG	CAGAGAATCGGGCGG	CTGGTGGAGCGGCTG	384

1 .	384	450	384	450	0	359	474	474	540	474	540	0	449	495	564	630	. 564	630
	Creerecaecre	CTGGTGGAGCGGCTG	CTGGTGGAGCGGCTG	CTGGTGGAGCGGCTG	5 526 540	GIGCIGGGCITCCIG GGCAGCICGICGGTG	GGCAGCTCGTCGGTG	GIGCIGGGCIICCIG GGCAGCICGICGGIG	GGCAGCTCGTCGGTG	GGCAGCTCGTCGGTG	GGCAGCTCGTCGGTG	616 630	TGGCTGTGTAAGATC		TGGCTGTGTAAGATC	TGGCTGTGTAAGATC	CAGAAGCGGCCCTG TGGCTGTGTAAGATC	TGGCTGTGTAAGATC
	CTGCAGGTCATCCAG AGGGCAGAGGGGCTC GACGTCCTGGAGCAG CAGAGAATCGGGCGG CTGGTGGAGCGGCTG	CAGAGAATCGGGCGG	CAGAGAATCGGGCGG	CAGAGAATCGGGCGG CTGGTGGAGCGGCTG	511 525	GIGCIGGGCITCCIG	CIGCICIGCGGGAG GIGCIGGGCTICCIG GGCAGCICGICGGIG		grecresectrects	GGCCTGTCCCAGTGT CTGCTCTGCGGGAG GTGCTGGGCTTCCTG GGCAGCTCGTCGTG	GGCCTGTCCCAGTGT CTGCTCTGCGGGGAG GTGCTGGGCTTCCTG GGCAGCTCGTCGTG	600 601 615	1 NOC2 TTCTGCAAAGACTGC AGGAAGAAAGTCTGC ACCAAATGTGGGATC GAGGCCTCCCCTGGC CAGAAGCGGCCCCTG TGGCTGTGTAAGATC		GAGGCCTCCCCTGGC CAGAAGCGGCCCCTG	CAGAAGCGGCCCCTG		GAGGCCTCCCTGGC CAGAAGCGGCCCCTG TGGCTGTAAGATC
	GACGTCCTGGAGCAG	CTGCAGGTCATCCAG AGGGCAGAGCGGCTC GACGTCCTGGAGCAG	GACGTCCTGGAGCAG	GACGICCIGGAGCAG	495 496 510	r crecrcreceeeaa	. CTGCTCTGCGGGAG	CTGCTCTGCGGGGAG	r crecrcrecesseas	CTGCTCTGCGGGGAG	CTGCTCTGCGGGGAG	586	SAGGCCTCCCCTGGC		GAGGCCTCCCCTGGC	: GAGGCCTCCCCTGGC	: GAGGCCTCCCCTGGC	; GAGGCCTCCCCTGGC
	AGGCCAGAGCGGCTC	AGGCAGAGCGGCTC	CTGCAGGTCATCCAG AGGGCAGAGCGGCTC	CTGCAGGTCATCCAG AGGGCAGAGCGGCTC	480 481 45	: Gecererecenere	AATGTGATGGGGAAC GGCCTGTCCCAGTGT	: GeccrercccAGTG1	: Geccrercccaerer	GGCCTGTCCCAGTGT	GGCCTGTCCCAGTGT	0 571 585	: ACCAAATGTGGGATC	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ACCAAATGTGGGATC	ACCAAATGTGGGATC	ACCAAATGTGGGATC	ACCAAATGTGGGATC
1				CTGCAGGTCATCCAG	466	AATGTGATGGGGAAG	AATGTGATGGGGAAC	AATGTGATGGGGAAC	AATGTGATGGGGAAC	AATGTGATGGGGAAC	AATGTGATGGGGAAC	556 570	AGGAAGAAAGTCTGG	AGGAAG	AGGAAGAAAGTCTGC	AGGAAGAAAGTCTGC	AGGAAGAAAGTCTGC	AGGAAGAAAGTCTGC
:	GAGGTGGAGGCCATC	GAGGTGGAGGCCATC	GAGGTGGAGGCCATC	GAGGTGGAGGCCATC	451 465	1 NOC2 GAGACCATGAGGGGG AATGTGATGGGGAAC GGCCTGTCCCAGTGT CTGCTTGCGGGGAG	2 NL1 GAGACCATGAGGCGG	3 LC1 GAGACCATGAGGCGG AATGTGATGGGGAAC GGCCTGTCCCAGTGT	GAGACCATGAGGCGG AATGTGATGGGGAAC	5 LC3 GAGACCATGAGGCGG	GAGACCATGAGGCGG AATGTGATGGGGAAC	541 555	TTCTGCAAAGACTGC	TTCTGCAAGACTGC AGGAAG-	TTCTGCAAAGACTGC	4 LC2 TTCTGCAAAGACTGC AGGAAGAAAGTCTGC	5 LC3 ITCTGCAAAGACTGC AGGAAGAAGTCTGC ACCAAATGTGGGATC	TTCTGCAAAGACTGC AGGAAGAAAGTCTGC ACCAAATGTGGGATC
•	3 LC1	4 LC2	5 LC3	6 LC4		1 NOC2	2 NL1	3 LC1	4 LC2	5 LC3	6 LC4		1 NOC2	2 NL1	3 LC1	4 LC2	5 LC3	6 LC4

	631 645	646 660	661	675 676 690	691 705 706	720	
1 NOC2	TGCAGTGAGCAAAGA	GAGGTCTGGAAGAGG	TCGGGGGCCTGGTTC	TACAAAGGGCTCCCC A	1 NOC2 TGCAGTGAGCAAAGA GAGGTCTGGAAGAGG TCGGGGGCCTGGTTC TACAAAGGGCTCCCC AAGTATATCTTGCCC CTGAAGACCCCTGGC	CTGGC	539.
2 NL1		GTCTGGAAGAGG	-GTCTGGAAGAGG TCGGGGGCCTGGTTC	TACAAAGGGCTCCCC A	TACAAAGGGCTCCCC AAGTATATCTTGCCC CTGAAGACCCCTGGC		567
3 LC1		GAGGTCTGGAAGAGG	TCGGGGGCCTGGTTC	TACAAAGGGCTCCCC A	TGCAGTGAGCAAAGA GAGGTCTGGAAGAGG TCGGGGGCCTGGTTC TACAAAGGGCTCCCC AAGTATATCTTGCCC CTGAAGACCCCTGGC	-	654
4 LC2	TGCAGTGAGCAAAGA	TGCAGTGAGCAAAGA GAGGTCTGGAAGAGG TCGGGGGGCCTGGTTC	TCGGGGGCCTGGTTC	TACAAAGGGCTCCCC AAGTATATCTTGCCC	AGTATATCTTGCCC CTGAAGACCCCTGGC		720
5 LC3	TGCAGTGAGCAAAGA	GAGGTCTGGAAGAGG	TCGGGGGCCTGGTTC	TACAAAGGGCTCCCC A	TECAGTGAGCAAAGA GAGGTCTGGAAGAGG TCGGGGGCCTGGTTC TACAAAGGGCTCCCC AAGTATATCTTGCCC CTGAAGACCCCTGGC		654
6 LC4		GAGGTCTGGAAGAGG	resesserestre	TACAAAGGGCTCCCC P	TGCAGTGAGCAAAGA GAGGTCTGGAAGAGG TCGGGGGCGTGGTTC TACAAAGGGCTCCCC AAGTATATCTTGCCC CTGAAGACCCCTGGC		720
	721 735	736	750 751 7.65	765 766 780 781	781 795 796	810	
1 NOC2	2 CGAGCTGATGACCCC	CACTTCCGACCTTTG	CCCACGGAACCGGCA	GAGCGAGAGCCCAGA	1 NOC2 CARGCTGATGACCCC CACTTCCGACCTTTG CCCACGGAACCGGCA GAGCGAGAGCCCAGA AGCTCTGAGACCAGC CGCATCTACACGTGG	ceree	629
2 NL1	CGAGCTGATGAGCCC	CAGITCCGACCITGG	CCCACGGAACCGGCA	GAGCGAGAGCCCAGA A	CAGITCCGACCITGG CCCACGGAACCGGCA GAGCGAGAGCCCAGA AGCTCTGAGACCAGC CGCAICTACACGTGG	ceree	657
3 LC1	CGAGCTGATGACCCC	CGAGCTGATGACCCC CACTTCCGACCTTTG	CCCACGGAACCGGCA	GAGCGAGAGCCCAGA	CCCACGGAACCGGCA GAGCGAGAGCCCAGA AGCTCTGAGACCAGC GGCATCTACACGTGG	CGTGG	744
4 LC2	4 LC2 CGAGCTGATGACCCC CACTTCCGACCTTTG	CACTTCCGACCTTTG	CCCACGGAACCGGCA	CCCACGGAACCGGCA GAGCGAGAGCCCAGA AGCTCTGAGACCAGC	AGCICTGAGACCAGC CGCATCTACACGTGG	ceree	810
.5 LC3	LC3 CGAGCTGATGACCCC CACTTCCGACCTTTG	CACTTCCGACCTTTG	CCCACGGAACCGGCA	CCCACGGAACCGGCA GAGCGAGAGCCCAGA AGCTCTGAGACCAGC	GCTCTGAGACCAGC CGCATCTACACGTGG	ceree	744
6 LC4	LC4 CGAGCTGATGACCCC CACTTCCGACCTTTG	CACTTCCGACCTTTG	CCCACGGAACCGGCA	GAGCGAGAGCCCAGA	CCCACGGAACCGGCA GAGCGAGAGCCCAGA AGCTCTGAGACCAGC CGCATCTACACGTGG	ceree	810
	811 825	826 840	3 841 855	5 856 870	871 885 886	006	
1 NOC2	1 NOC2 GCCCGAGGAAGAGT-	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			!	643
2 NL1	2 NL1 GCCCGAGGAAGAGT-	1					671
3 1.01	3 LC1 GCCCGAGGAAGAGT-			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			758
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	824	834	006		689	717	804	870	924	066		779	807	894	960
:	1 1	AAGCCGG	AAGCCGG	066	CTCCAGC	CTCCAGC	CTCCAGC	CTCCAGC	CTCCAGC	CTCCAGC	1080	CCCCAGG	cccAGG	cccAGG	cccAGG
,	 	AGTGGAAG	AGTGGAAĞ	976	CTTAGCTC	GACAGIGACTCGGAT CTTAGCTCCTCCAGC	CTTAGCTCCTCCAGC	CTTAGCTCCTCCAGC	CTTAGCTCCTCCAGC	CTTAGCTCCTCCAGC	1065 1066	GTGGAGGC	GTGGAGGC	GTGGAGGCCCCCAGG	GTGGAGGCCCCCAGG
	1	CCATGCGA	ccarecea	975	ACTCGGAT	ACTCGGAT	ACTCGGAT	ACTCGGAT	ACTCGGAT	ACTCGGAT	1065	GTGGCAGC	TGGCAGC	STGGCAGC	
		r gaaaaca	r gaaaaca	960 961	-G GTTTCCAGTGACAGT GACAGTGACTCGGAT CTTAGCTCCTCCAGC	GACAGTG	GTTTCCAĞTGACAGT GACAGTGACTCGGAT	GITTCCAGTGACAGT GACAGTGACTCGGAT	GTTTCCAGTGACAGT GACAGTGACTCGGAT	GACAGTG	1050 1051	s GAGTCAG	GAGTCAG	GACAAACCCTGGAAG GAGTCAGGTGGCAGC	GAGTCAGG
		теавтсст	тсастсст	96	:AGTGACAG	GTTTCCAGTGACAGT	AĞTGACAGI	AGTGACAGI	AGTGACAGI	AGTGACAGI	105	CCCTGGAAG	CCTGGAAG	CCTGGAAG	CCTGGAAG
f.	}	G CCTGGA	G CCTGGA	945 946	G GTTTCC	-G GTTTCC	G GTTTCC	-G GTTTCC	G GTTTCC	G GTTTCC	1035 1036	C GACAAA	C GACAAA	c GACAAA	C GACAAA
	ő	GTAGGAAGAAAGTGC TGATCCACGCTGCAG CCTGGATGAGTCCTT GAAAACACCCATGCGA AGTGGAAGAAGCGG	CACGCTGCA	6	! ! !	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	9-	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ATGAGCAGT	TGTTGTGTGATCTCA TCTATATGAGCAGTG GTTTCCAGTGACAGT GACAGTGACTCGGAT	103	CCATCCACTGGGGGTC AGGGAAAAGGC GACAAACCCTGGAAG GAGTCAGGTGGCAGC GTGGAGGCCCCCAGG	CCATCCACTGGGGTC AGGGACCGGAAAGGC GACAAACCCTGGAAG GAGTCAGGTGGCAGC GTGGAGGCCCCCAGG	AGGGACCGGAAAGGC	CCATCCACTGGGGTC AGGGACCGGAAAGGC GACAAACCCTGGAAG GAGTCAGGTGGCAGC
		C TGATC	C TGATO	930 931		1		-	A TCTAT	A TCTAT	1020 1021	C AGGGA	C AGGGA	C AGGGA	C AGGGA
	1	aagaaagto	aagaaagto	, o					rgrgarcró	rergarere	100	cacreeeed	zacregeer	CCATCCACTGGGGTC	ACTGGGGT
		GTAGG	GTAGG	5 916	1		1		TGTTG		5 1006				
٠.	LC2 GCCCGAGGAAGAGT-	LC3 GCCCGAGGAAGAGTC	6 LC4 GCCCGAGGAAGAGTC GTAGGAAGAAAGTGC TGATCCACGCTGCAG CCTGGATGAGTCCTT GAAAACACCATGCGA AGTGGAAGAAGCCGG	91.		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1	AGACGAAAGGCCGCC TGTTGTGTGATCTCA TCTATATGAGCAGTG	AGACGAAAGGCCGCG	100	1 NOC2 CTAGAGGACAGACTC	CTAGAGGACAGACTC	CTAGAGGACAGACTC	CTAGAGGACAGACTC
	90009	90009	၅၃၁၁၅	901	1	1	1 1	1		AGACG,	991	CTAGA			
	LC2	5 LC3	LC4		1 NOC2	NL1	12	4 LC2	1,03	6 LC4		NOC2	NL1	roj	172
	4	S	9			7	m	4	'n	9		-	7	٣	4

1014	1080		847	168	984	1050	1104	1170	
GTGGAGGCCCCCAGG	GTGGAGGCCCCCAGG	1155 1156 1170	1 1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	TCTGCTGACCCGCCA	rcrecreaccecca	TCTGCTGACCCGCCA	TCTGCTGACCCGCCA		
GAGTCAGGTGGCAGC	GAGTCAGGTGGCAGC	1140 1141 1155	GAGACGGG	CCCGCGGGCCACCTC TTTGGGTTGCAGAGC AGCCTGGCCAGTGGT GAGACGGGCACAGGC TCTGCTGACCGGCCA	CCCGCGGGCCACCTC 1TTGGGTTGCAGAGC AGCCTGGCCAGTGGT GAGACGGGCACAGGC TCTGCTGACCGGCCA	CCCGCGGGCCACCIC TITGGGTTGCAGAGC AGCCTGGCCAGTGGT GAGACGGGCACAGGC ICTGCTGACCGGCCA	GAGACGGGCACAGGC	GAGACGGGCACAGGC	
GACAAACCCTGGAAG	GACAAACCCTGGAAG	1125 1126 1140	AGCCTGGCCAGTGGT	AGCCTGGCCAGTGGT	AGCCTGGCCAGTGGT	AGCCTGGCCAGTGGT	AGCCTGGCCAGTGGT	AGCCTGGCCAGTGGT	
AGGGACCGGAAAGGC	AGGGACCGGAAAGGC	1110 1111 1125	TCTGGGTGCCAGAGC	TTTGGGTTGCAGAGC	TTTGGGTTGCAGAGC	TTTGGGTTGCAGAGC	TTTGGGTTGCAGAGC	TTTGGGTTGCAGAGC	
CCATCCACTGGGGTC	CCATCCACTGGGGTC	095 1096 1110	CCGCCGGGCCACCTC	CCCGCGGGCCACCTC	CCCGCGGGCCACCTC	CCCGCGGGCCACCTC	CCCGCGGCCACCTC	ccceceeeccaccic	
5 LC3 CTAGAGGACAGACTC CCATCCACTGGGGTC AGGGACCGGAAAGGC GACAAACCCTGGAAG GAGTCAGGTGGCAGC GTGGAGGCCCCCAGG	6 LC4 CTAGAGGACAGACTC CCATCCACTGGGGTC AGGGACCGGAAAGGC GACAAACCCTGGAAG GAGTCAGGTGGCAGC GTGGAGGCCCCCAGG	1081 1095	1_NOC2 ATGGGGTTCACCCAC CCGCCGGGCCACCTC TCTGGGTGCCAGAGC AGCCTGGCCAGTGGT GAGACGGG	2 NL1 ATGGGGTTCACCCAA	3 LCI ATGGGGTTCACCCAA	4 LC2 ATGGGGTTCACCCAA	S LC3 ATGGGGTTCACCCAA CCCGCGGGCCACCTC TTTGGGTTGCAGAGC AGCCTGGCCAGTGGT GAGACGGGCACAGGC TCTGCTGACCGGCCA	6 LC4 ATGGGGTTCACCCAA CCCGCGGGCCACCTC TTTGGGTTGCAGAGC AGCCTGGCCAGTGGT GAGACGGGCACAGGC TCTGCTGACCGGCCA	
5 LC3	6 LC4		1 NOC2	2. NL1	3 LC1	4 LC2	5 LC3	6 LC4	

	1171 1185	1185 1186 1200	1200 1201 1215	1215 1216 1230	1230 1231 124	1245 1246 1260	0
NOC2	GACAGGC	TCTGCTGACCCGCCA	GGGGACCCCGCCCC	GGGCTGACCCGAAGG	GCCCCGGTAAAAGAC	NOC2GACAGGC TCTGCTGACCCGCCA GGGGGACCCCGCCC GGGCTGACCCGGAAGG GCCCCGGTAAAAGAC ACACCTGGACGAGCC	929
NL1	GGGGGAGGGACAGGC	TCTGCTGACCCGCCA	GGGGGACCCCGCCCC	GGGCTGACCCGAAGG	GCCCGGTAAAAGAC	NL1 GGGGGAGGGACAGGC TCTGCTGACCCGCCA GGGGGACCCCGCCG GGGCTGACCCGGAAGG GCCCGGTAAAAGAC ACACCTGGACGAGCC	987
Σ	GGGGGAGGGACAGGC	TCTGCTGACCCGCCA	GGGGGACCCCGCCCC	GGGCTGACCCGAAGG	GCCCCGGGTAAAAGAC	LC1 GGGGGAGGGACAGGC TCTGCTGACCCGCCA GGGGGACCCCGCCCC GGGTGACCCGAAGG GCCCCGGTAAAAGAC ACACCTGGACGAGCC	1074
LC2	GGGGGAGGGACAGGC	TCTGCTGACCCGCCA	GGGGGACCCCGCCCC	GGGCTGACCCGAAGG	GCCCCGGTAAAGAC	LC2 GGGGGAGGGACAGGC TCTGCTGACCCGCCA GGGGGACCCCGCCGGGGACCCGGAAGG GCCCGGTAAAAGAC ACACCTGGACGAGCC	1140
LC3	GGGGGAGGGACAGGC	TCTGCTGACCCGCCA	GGGGGACCCCGCCCC	GGGCTGACCCGAAGG	GCCCCGGTAAAAGAC	LC3 GGGGGAGGGACAGGC TCTGCTGACCCGCCA GGGGGACCCCGCCC GGGCTGACCCGGAAGG GCCCCGGTAAAAGAC ACACCTGGACGAGCC	1194
IC4	GGGGGGGGACAGGC	TCTGCTGACCCGCCA	GGGGACCCCGCCCC	GGGCTGACCCGAAGG	GCCCCGGTAAAAGAC	1C4 GGGGGGGGGACAGGC TCTGCTGACCCGCCA GGGGGACCCCGCCC GGGCTGACCCGAAGG GCCCCGGTAAAAGA ACACCTGGACGAGCC	1260

	1019	1077	1164	1230	1284	1350		1109	1167	1254	1320	1374	1440	
1350							40		11 . 2					
13	ATTCC	TTC	TTCCI	TTCCI	תדככו	TTCCI	1440	3GGAG	GGAGC	эселес	GGAGG	GGAGG	GGAGG	
	3GAGG/	GAGGA	GAGGA	GAGGA	GAGGA	GAGGA	٠.	FGTT	TGTTG	TGTT	TGTT	TGTT	TGTTG	
1335 1336	CTGT	CTGTG	crere	CTGTG	crere	crere	1425 1426	ACCAC	ACCAG	ACCAG	ACCAG	ACCAG	ACCAG	
1335	TTCC	TTCC	TTCC	TTCC	TTCC	TTCC	1425	ACAA	ACAA	ACAA	ACAA	ACAA	ACAA	
	CAGAC	CAGAC	CAGAC	CAGAC	CAGAC	CAGAC		ACTOR	ACTCA	ACTCA	ACTCA	ACTCA	ACTCA	
1321	CTGGA	TGGAA	TGGAA	TGGAA	TGGAA	TGGAA	1411	SCCATO	CCATG	CCATG	CCATG	CCATG	CCATG	
1320 1321	GTGC (TGC C	FTGC C	FTGC O	FIGC C	FGC C	1410-1411	STTG (TTG G	TTG G	TTG G	TTG G	FTTG G	
	GTCTG	srċrec	STCTG	srcre	FTCTG	अत्तराक्त		ACCCT	ACCCTO	ACCCTC	ACCCTO	ACCCT	ACCCTG	
306	1 NOC2 CCGGCTGCTGACGCA GCTCCAGCAGGCCCC TCCAGCTGCCTGGGC TGAGGTGTCTGGTGC CTGGAACAGACTTCC CTGTGGAGGATTCCT	2 NL1 CCCGCTGCTGACGCA GCTCCAGCAGGCCCC TCCAGCTGCTGGGC TGAGGTGTCTGGTGC CTGGAACAGACTTCC CTGTGGAGGATTCCT	3 LC1 CCGGTGCTGACGCA GCTCCAGCAGGCCCC TCCAGCTGCCTGGGC TGAGGTGTCTGGTGC CTGGAACAGACTTCC CTGTGGAGGATTCCT	4 LC2 CCCGCTGCTGACGCA GCTCCAGCAGGCCCC TCCAGCTGCCTGGGC TGAGGTGTCTGGTGC CTGGAACAGACTTCC CTGTGGAGGATTCCT	5 LC3 CCCGCTGCTGAACGCA GCTCCAGCAGGCCCC TCCAGCTGCGCT TGAGGTGTCTGGTGC CTGGAACAGACTTCC CTGTGGAGGATTCCT	6 LC4 CCCGCTGCTGACGCA GCTCCAGCAGGCCCC TCCAGCTGCCTGGGC TGAGGTGTCTGGTGC CTGGAACAGACTTCC CTGTGGAGGATTCCT	396	1 NOC2 GCCAGACCTGCCCG GCTCCTCCCTGACCG GTCCTTGTGCCCTCA CCAGACACCCTGTTG GCCATGACTCAACAA ACCAGTGTTGGGAGC	2 NL1 GCCAGACCCTGCCCG GCTCCTCCTGACCG GTCCTTGTGCCCTCA CCAGACACCCTGTTG GCCATGACTCAACAA ACCAGTGTTGGGAGC	3 LC1 GCCAGACCCTGCCCG GCTCCTGACCG GTCCTTGTGCCCTCA CCAGACACCCTGTTG GCCATGACTCAACAA ACCAGTGTTGGGAGC	4 LC2 GCCAGACCCTGCCCG GCTCCTCCTGACCG GTCCTTGTGCCCTCA CCAGACACCCTGTTG GCCATGACTCAACAA ACCAGTGTTGGGAGC	LC3 GCCAGACCCTGCCCG GCTCCTCCTGACCG GTCCTTGTGCCCTCA CCAGACACCCTGTTG GCCATGACTCAACAA ACCAGTGTTGGGAGC	6 LC4 GCCAGACCCTGCCCG GCTCCTCCTGACCG GTCCTTGTGCCCTCA CCAGACACCCTGTTG GCCATGACTCAACAA ACCAGTGTTGGGAGC	
1305 1306	3660 1	iggc T	GGC T	AGC T	16GC T	T 299	1395 1396	orca o	TCA C	TCA C	TCA C	TCA C	TCA C	
	TGCCT	record	recen	GCCTC	GCCTG	GCCTG		3TGCC	FECC	FECCO	FECC	TGCCC	FGCCC	
. 162	CCAGC	CCAGC	CCAGC	CCAGC	CCAGC	CCAGC	381	TCCTT	TCCTT	TCCTT	TCCTT	TCCTT	TCCLT	
1290 1291	2000	T CCC	CCC	CCC I	ترد ب <u>ا</u> درد	ř CCC	1380 1381		, 9 9 9 9	ອ. ອວວ		CCG G	9 9 9	
	CAGGC	CAGGC	CAGGC	CAGGC	CAGGC	CAGGC	-	CCTGA	CCTGA	CCTGÄ	CCTGA	CCTGA	CCTGA	
276	TCCAG	TCCAG	TCCAG	TCCAG	TCCAG	TCCAG	366	TCCTC	TCCTĊ	TCCTG	TCCTC	TCCTO	TCCTC	
275 1276	£5.	ე _წ	ე _ნ •ა	ეგ ტე	SP GC	CA GC	365 1366) 90	<u> </u>	ටුල ලට	ည	ည	ည	
. 	TGACC	TGACG	TGACG	TGACG	TGACG	TGACG	Ä	CTGCC	CTGCC	CTGCC	CTGCC	CTGCC	CTGCC	
	GCTGC	GCTGC	GCTGC	GCTGC	GCTGC	сст вс		AGACC	AGACC	AGACC	AGACC	AGACC	AGACC	
1261	, ccc	ပ္ပ	ပ္ပ	DD -	9	Ö	1351	.2 GCC	900	229	ည	228	90	
	1 NOC	2 NL1	3 LC1	4 LC2	5 [C3	6 LC4	•	1 NOC	2 NL1	3 LC1	4 LC2	5 LC3	6 LC4	

3 LC1 GICTGCCTCCCCAG CTCAGTGCCTTTCTG CACCCCTTCTCTCT GGGAGCTGTCTGCA TCCGCCACCCCTCC AACCACTGCCTCAG 1344 1 NOC2 CGTCTGCCTCCCCAG CTCAGTGCCTTTCTG CACCCCTTCTCTCT GGGAGCTGTCTGCA TCCGCCACCCCTCC AACCACTGCCTCAG 1199 2 NL1 CGICTGCCTCCCAG CICAGIGCCTITICIG CACCCCTTCTCTCT GGGAGCTGTCTGCA ICCGCCACCCCCTCC AACCACTGCCCTCAG 1257 1500 1501 1515 1516 1455 1456 1470 1471 1485 1486

	1410	1464	1530
	4 LC2 CGTCTGCCTCCCCAG CTCAGTGCCTTTCTG CACCCCTTCTCTCT GGGGAGCTGTCTGCA TCCGCCACCCCCTCC AACCACTGCCCTCAG 1410	5 LC3 CSTCTGCCTCCCCAG CTCAGTGCCTTTCTG CACCCCTTCTCTCT GGGGAGCTGTCTGCA TCCGCCACCCCTCC AACCACTGCCTCAG 1464	6 LC4 CGTCTGCCTCCCCAG CTCAGTGCCTTTCTG CACCCCTTCTCTCT GGGGAGCTGTCTGCA TCCGCCACCCCCTCC AACCACTGCCCTCAG 1530
	TCCGCCACCCCCTCC	TCCGCCACCCCCTCC	TCCGCCACCCCCTCC
,	GGGGAGCTGTCTGCA	GGGGAGCTGTCTGCA	GGGGAGCTGTCTGCA
	CACCCTTCTCTCCT	CACCCTTCTCTCT	CACCCTTCTCTCT
	rcaereccificte	STCAGTGCCTTTCTG	CICAGTGCCTTTCTG
	CGTCTGCCTCCCCAG (CGTCTGCCTCCCCAG (CGTCTGCCTCCCCAG (
	4 LC2	5 LC3 (6 LC4

		1289	1347	1434	1500	1554	1620		1379	1437	1524	1590	1644	1710	
	1605 1606 1620	TTGGGTTGGG	Tracerracecrace	TTGGGTTGGGCTGGG	TTGGGTTGGGCTGGG	TTGGGTTGGG	TTGGGTTGGGCTGGG	1695 1696 1710	TGAAACCTAGGGCAC	TGAAACCTAGGGCAC	TGAAACCTAGGGCAC	TGAAACCTAGGGCAC	TGAAACCTAGGGCAC		
	1590 1591 1605	AAGTTTGCGCGTGTC	CCCCCGACCTTATTI ATTACCCTCC CACACCCCCAATCTA CCTGGTGATGTTT AAGTTTGCGCGTGTC TTGGGTTGGG	AAGTTTGCGCGTGTC	AAGTTTGCGCGTGTC	AAGTTTGCGCGTGTC	AAGTTTGCGCGTGTC	1680 1681 1695	AATGGCAAGACTAAA	AATGGCAAGACTAAA	AATGGCAAGACTAAA	AATGGCAAGACTAAA	CTCCGTTGCTATAIT AATGGCAAGACTAAA TGAAACCTAGGGCAC	AATGGCAAGACTAAA	
	1575 1576 1590	CCTGGTGATGATTTT	CCTGGTGATGATTTT	CCTGGTGATGATTTT	CCTGGTGATGATTTT	CCTGGTGATGATTT	CCTGGTGATGATTTT	1665 1666 1680	CTCCGTTGCTATATT	CTCCGTTGCTATATT	CTCCGTTGCTATATT	CTCCGTTGCTATATT	CTCCGTTGCTATATT	CTCCGTTGCTATATT	
•	1560 1561 1575	CACACCCCCAATCTA	CACACCCCCAATCTA	CACACCCCCAATCTA	CACACCCCCAATCTA	CACACCCCCAATCTA	CACACCCCCAATCTA	1650 1651 1665	GCCCGGTGGGGCTAT	GCCCGGTGGGGCTAT	GCCCGGTGGGGCTAT	GCCCGGTGGGGCTAT	GCCCGGTGGGGCTAT	GCCCGGTGGGGCTAT	
	1545 1546 1560	ATTACCCTCCCCTCC	ATTACCCTCCCCTCC	ATTACCCTCCCTCC	ATTACCCTCCCTCC	ATTACCCTCCCTCC	ATTACCCTCCCCTCC	1635 1636 1650	AGTGTCAGAGGGGCC	AGTGTCAGAGGGGCC	AGTGTCAGAGGGGCC	AGTGTCAGAGGGGCC	AGTGTCAGAGGGGCC	AGTGTCAGAGGGGCC	
	1531 1545	1 NOC2 CCCCCGACGITAITI ATTACCCTCCCCTCC CACACCCCCAATCIA CCTGGTGATGATTTT AAGTITGCGCGTGTC TIGGGTTGGGCTGGG	CCCCCGACCTTATTT	3 LC1 CCCCGACCTIATIT ATTACCCTCC CACACCCCCAATCTA CCTGGTGATGATTT AAGTTTGCGCGTGTC TTGGGTTGGG	4 LC2 CCCCGACCTTATTT ATTACCCTCCCTCC CACACCCCCAATCTA CCTGGTGATTTT AAGTTTGCGCGTGTC TTGGGTTGGG	5 LC3 CCCCGACCTTATTT ATTACCCTCC CACACCCCCAALCTA CCTGGTGATGATTT AAGTTTGCGCGTGTC TTGGGTTGGG	6 LC4 CCCCCGACCTTAITT ATTACCCTCCCTCC CACACCCCCAATCTA CCTGGTGATTTT AAGTTTGCGCGTGTC TTGGGTTGGG	1621 1635	1 NOC2 GGGTTTCCCACATGC AGTGTCAGAGGGGCC GCCCGGTGGGGCTAT CTCCGTTGCTATATT AATGGCAAGACTAAA TGAAACCTAGGGCAC	2 NLI GGGTTTCCCACATGC AGTGTCAGAGGGCC GCCCGGTGGGGCTAT CTCCGTTGCTATATT AATGGCAAGACTAAA TGAAACCTAGGGCAC	3 LC1 GGGTTTCCCACATGC AGTGTCAGAGGGCC GCCCGGTGGGGCTAT CTCCGTTGCTATATT AATGGCAAGACTAAA TGAAACCTAGGGCAC	4 LC2 GGGTTTCCCACATGC AGTGTCAGAGGGGCC GCCCGGTGGGGCTAT CTCCGTTGCTATATT AATGGCAAGACTAAA TGAAACCTAGGGCAC	5 LC3 GGGTTTCCCACATGC AGTGTCAGAGGGCC GCCCGGTGGGGCTAT	6 LC4 GGGTITCCCACAIGC AGIGTCAGAGGGGCC GCCCGGTGGGGCTAI CTCCGTIGCTATAIT AATGGCAAGACTAAA TGAAACCTAGGGCAC	
		1 NOC2	2 NL1	3 LC1	4 LC2	5 LC3	6 LC4		1 NOC2	2 NLI	3 LC1	4 LC2	5 1.03	6 LC4	

	1469.	1527	1614	1680	1734	1800			1559	1617	1704	1770	1824	1890		1649	1707	
1800	CICCCIIC	CTCCCTTC		Tereceretecerre	CTCCCTTC	CTCCCTTC		1890	TGGTTTT	TGGTTTT	TGGTTTTT	TGGTTTTT	GTTTCTTTGGTTTTT		1980	CCACCTCC		
1785 1786	TCTCCCT	TCTCCCT	rcrccr	TCTCCCT	TCTCCCT	TCTCCCT	-	1876	GTTTCTT	GTTTCTT	GTTTCTT	GTTTCTT	GTTTCTT	GTTTCTT	1966	GCAACCT	GCAACCT	٠
1785	CACCCACCC	PACCACCC	PACCCACCC	PACCCACCC	GAGACTCACCCACCC TCTCCCTCTCCCTTC	PACCCACCC		1875	GTCTGTTTA	FICTGTTTA	STCTGTTTA	STCTGTTTA		TCTGTTTA	1965	GGCTCACT	GGCTCACT	
1770 1771	GAGACT	GAGACT	GAGACTO	GAGACTO	GAGACT	GAGACT	-	1861	ACCTGG	ACCTGG	ACCTGG	AccTGG	ACCTGGG	ACCTGG	1951	CGATCG	CGATCGC	
177(SCAGTGAGGGG	CAGTGAGGGG	CAGTGAGGGG	CAGTGAGGGG	CAGTGAGGGG	CAGTGAGGGG		1860	CGCGGGTGAA	CGCGGGTGAA	CGCGGGTGAA	CGCGGGTGAA	ceceeereAA	CGCGGGTGAA	1950	TGCAGTGGCA	recaereeca	•
1755 1756	CAGAG	CAGAG	CAGAG	CAGAG	CAGAG	CAGAG		1846	AGGAC	AGGAC	AGGAC	AGGAC	AGGAC	AGGAC	5 1936	TGGGG	TGGGG	
	GIGIGGCCCCTIAGA GGIGAGCAICAGAGC CAGAGCAGIGAGGGG GAGACICACCCACCC ICICCCICICCTIC	GIGIGGCCCCTIAGA GGTGAGCATCAGAGC CAGAGCAGTGAGGGG GAGACTCACCCACCC TCTCCCTCTCCCTTC	GIGIGGCCCTIAGA GGIGAGCAICAGAGC CAGAGCAGIGAGGGG GAGACICACCCACCC ICICCCICICCTIC	GGTGAGCATCAGAGC CAGAGCAGTGAGGGG GAGACTCACCCACGC	GTGTGGCCCCTTAGA GGTGAGCATCAGAGC CAGAGCAGTGAGGGG	GIGIGGCCCTITAGA GGIGAGCAICAGAGC CAGAGCAGIGAGGG GAGACICACCCACCC ICICCCICICCCTIC		1 1845	GCGCAGTGCCCCCT CCCATGGGCTGGCCC AGGACCGCGGGTGAA ACCTGGGTCTGTTA GTTTCTTTGGTTTTT	gcgcagtgcccccct cccatgggctggccc aggaccgcgggtgaa acctgggtctgttta gtttctttggtttt	GCGCAGIGCCCCCCI CCCAIGGGCIGGCCC AGGACCGCGGGIGAA ACCIGGGICIGIIIA GIIICIIIGGIIIII	GCGCAGTGCCCCCT CCCATGGGCTGGCC AGGACCGCGGTGAA ACCTGGGTCTGTTA GTTTCTTTGGTTTT	GCGCAGTGCCCCCCT CCCATGGGCTGGCC AGGACCGCGGGTGAA ACCTGGGTCTGTTTA	CCCATGGGCTGGCCC AGGACCGCGGGTGAA ACCTGGGTCTGTTTA GTTTCTTTGGTTTTT	1935	TTTGACACAGTCTCG CTTTGTTGCCCAGGC TGGGGTGCAGTGGCA CGATCGCGGCTCACT GCAACCTCCACTCC	TTTGACACACTOTOG CTTTGTTGCCCAGGC TGGGGTGCAGTGGCA CGATCGCGGCTCACT GCAACCTCCACTCC	
0 1741	A GGT(A GGTG	A GGTG	A GGT€	A GGT€	A GGTC		0 1831	T. CCC.	, r	r ccc	r CCC	CCCA	CCCA	1920 1921	CTTI	CTTT	
6 1740	GGCCCTTAG	GGCCCCTTAG?	Geccettas.	GTGTGGCCCCTTAGA	GGCCCCTTAG?	GGCCCCTTAG?		6 1830	AGTGCCCCC	AGTGCCCCCC	AGTGCCCCCC	AGTGCCCCCC	AGTGCCCCCCT	GCGCAGTGCCCCCT		ACACAGTCTCC	ACACAGTCTCG	
5 1726				_				5 1816							5.1906			
1725	1 NOC2 GECCTCCGAAGCTGC	2 NL1 GGCCTCCGAAGCTGC	3 LCI GGCCTCCGAAGCTGC	4 LC2 GGCCTCCGAAGCTGC	5 LC3 GGCCTCCGAAGCTGC	6 LC4 GGCCTCCGAAGCTGC	•	1815	1 NOC2 AGCTCTGGGAGGCAG	2 NL1 AGCTCTGGGAGGCAG	3 LC1 AGCTCTGGGAGGCAG	4 LC2 AGCTCTGGGAGGCAG	5 LC3 AGCTCTGGGAGGCAG	6 LC4 AGCTCTGGGAGGCAG	1905	1 NOC2 GTATGTTTGTTTGTT	2 NL1 GTATGTTTGTTTGTT	
1711	GGCCT	GGCCT	GGCCT	GGCCT	GGCCT	GGCCT		1801	AGCTC	AGCTC	AGCTC	AGCTC	AGCTC	AGCTC	1891	GTATG	GTATG	
•	1 NOC2	2 NL1	3 LCI	4 LC2	5 LC3	· 6 LC4			1 NOC2	2 NL1	3 LC1	4 LC2	5 LC3	6 LC4	•	1 NOC2	2 NL1	

	1794	1860	1914	1980			1739	1797
	GCAACCTCCACCTCC	GCAACCTCCACCTCC	GCAACCTCCACCTCC	GCAACCTCCACCTCC		2055 2056 2070	TTTTTGTATTTTAG	TTTTTGTATTTTAG
1	CGATCGCGGCTCACT	CGATCGCGGCTCACT	CGATCGCGGCTCACT	CGATCGCGGCTCACT	·	2040 2041 2055	ACCACACCCAGTTAA	ACCACACCCAGTTAA
	TGGGGTGCAGTGGCA	TGGGGTGCAGTGGCA	TGGGGTGCAGTGGCA	TGGGGTGCAGTGGCA		2025 2026 2040	TTACAGATGCCCGCC	TTACAGATGCCCGCC
	CTTTGTTGCCCAGGC	CTTTGTTGCCCAGGC	CTTTGTTGCCCAGGC	CTTTGTTGCCCAGGC		2010 2011 2025	CCTGAGTAGGTGGGA	CCTGAGTAGGTGGGA
· .	TTTGACACAGTCTCG	TTTGACACAGTCTCG	TTTGACACAGTCTCG	TTTGACACAGTCTCG		1995 1996 2010	CTCTCACCTCAGCCT	crcrcaccrcagccr
	3 LC1 GIATGITTGITTGIT ITTGACACAGICTCG CITTGITGCCCAGGC TGGGGTGCAGTGGCA CGATCGCGGCTCACT GCAACCTCCACTCC	4 LC2 GTATGTTTGTTTGTT TITGACACAGTCTGG CTTTGTTGCCCAGGC TGGGGTGCAGTGGCA CGATCGCGGCTCACT GCAACCTCCACTCC	5 LC3 GTATGTTTGTTTTTGACACAGACTCG CTTTGTTGCCCAGGC TGGGGTGCAGTGGCA CGATCGCGGCTCACT GCAACCTCCACTC	GTAIGTITGIII IIIGACACAGICICG CITIGIIGCCCAGGC IGGGGIGCAGIGGCA CGAICGCGGCICACI GCAACCICCACICC		1981 1995	1 NOC2 CGGGCTCAAGCGATT CTCTCACCTCAGCCT CCTGAGTAGGTGGGGA TTACAGATGCCCGCC ACCACACCAGTTAA TTTTTGTATTTTAG	2 NL1 CGGGCTCAAGCGATT CTCTCACCTCAGCCT CCTGAGTAGGTGGGA TTACAGATGCCCGCC ACCACACCCAGTTAA TTTTTGTATTTTTAG
	3 LC1	4 LC2	5 LC3	6 LC4			1 NOC2	2 NL1

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1914	1980			1739	1797	1884	1950	2004	2070			1829	1887	1974	2040					
TCCACCTCC	STCCACCTCC		2070	GTATTTTAG	STATTTTAG	STATTTTAG	GTATTTTAG	GTATTTTAG	GTATTTTAG		2160	AGTGCTGGGA	AGTGCTGGGA	AGTGCTGGGA	AGTGCTGGGA				-	
GCAAC	GCAAC		2056	TTTT	TTTT	TTTT	TTTT	TTTT	TTTT		2145 2146	CCCA	CCCAA	CCCAA	CCCAA					
GGCTCACT	GGCTCACT		2055	CCAGTTAA	CCAGTTAA	CCAGTTAR	CCAGTTAA	CCAGTTAA	CCAGTTAA		2148	CCTCGGCCT	CTCGGCCT	creecer	CTCGGCCT					
SGATCGC	SGATCGC		2040 2041	ACCACA	ACCACAC	ACCACAC	ACCACAC	ACCACAC	ACCACAC		2130 2131	CGCCCG	ceccce	دودددود	כפכככפכ	•				
GCAGTGGCA	GCAGTGGCA (2040	PATGCCCGCC	ATGCCCGC	ATGCCCGCC	ATGCCCGCC	ATGCCCGCC	ATGCCCGCC		٠.	TCAAGTGATC	CAAGTGATC	CAAGTGATC	CAAGTGATC					
TĠGGGT	TGGGGT	•	2025 2026	TTACAC	TTACAG	TTACAG	TTACAG	TTACAG	TTACAC		2115 2116	TGGTC	TGGTCI	TGGTCT	regra					
rttettecccaggc	гттеттесссявес	٠		CTGAGTAGGTGGGA	CTGAGTAGGTGGGA	CTGAGTAGGTGGGA	CTGAGTAGGTGGGA	CTGAGTAGGTGGGA	CTGAGTAGGTGGGA			TGGTCTTGAACTCC	TGGTCTTGAACTCC	TGGTCTTGAACTCC	TGGTCTTGAACTCC					
TITGACACAGICICG CIIIGIIGCCCAGGC IGGGGIGCAGIGGCA CGAICGCGGCTCACT GCAACCICCACCICC	TITGACACAGICICG CITIGIIGCCCAGGC IGGGIGCAGIGGCA CGAICGCGGCICACI GCAACCICCACICC		96 2010 2011	CTCTCACCTCAGCCT CCTGAGTAGGTGGGGA TTACAGATGCCCGCC ACCACACCCCAGTTAA TTTTTGTATTTTTAG	CICICACCICAGCCI CCIGAGIAGGIGGGA TIACAGAIGCCCGCC ACCACACCCCAGIIAA ITITIGIAITITIAG	CICTCACCTCAGCCT CCTGAGIAGGIAGGIGGGA TIACAGAIGCCCGCC ACCACACCCAGTIAA IITITGIAITITIAG	CTCTCACCTCAGCCT CCTGAGTAGGTGGGGA TTACAGATGCCCGCC ACCACACCCAGTTAA TTTTTGTATTTTTAG	CTCTCACCTCAGCCT CCTGAGTAGGTGGGA TTACAGATGCCCGCC ACCACACCCCAGTTAA TTTTTGTATTTTTAG	CTCTCACCTCAGCCT CCTGAGTAGGTGGGGA TTACAGATGCCCGCC ACCACACCCAGTTAA TTTTTGTATTTTTAG		2086 2100 2101	NOC2 AAGAGATGGGGTTTC TCCATGTTGGCCAGG CTGGTCTTGAACTCC TGGTCTCAAGTGATC CGCCCGCCTCGGCCT CCCAAAGTGCTGGGA	ICCAIGIIGGCCAGG CIGGICIIGAACICC IGGICICAAGIGAIC CGCCCGCCICGGCCI CCCAAAGIGCIGGGA	TOCATGTIGGCCAGG CTGGTCTTGAACTCC TGGTCTCAAGTGATC CGCCCGCCTCGGCCT CCCAAAGTGCTGGGA	4 LC2 AAGAGATGGGGTTTC TCCATGTTGGCCAGG CTGGTCTTGAACTCC TGGTCTCAAGTGATC CGCCCGCCTCGGCCT CCCAAAGTGCTGGGA					
		•	1995 1996	£				_	E.,		S	TC TC	TC TCC		TC TCC					
S LC3 GTATGTTTGTTTGTT	S LC4 GTATGTTTGTTTGTT		1981	NOC2 CGGGCTCAAGCGATI	2 NL1 CGGGCTCAAGCGATT	CGGGCTCAAGCGATT	4 LC2 CGGGCTCAAGCGATT	5 LC3 CGGGCTCAAGCGATT	6 LC4 CGGGCTCAAGCGAT1	e Sest	2071 208	AAGAGATGGGGTT	2 NL1 AAGAGATGGGGTTTC	3 LC1 AAGAGATGGGGTTTC	AAGAGATGGGGTT"					
LC3	LC4			NOC2	NL1	3 LC1	LC2	; IC3	LC4			NOC2	NL1	1C1	rc5		•			
- 10	10				~	~	マ	ເກ	v	•			~~	(7)	4					

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* 007	2070			1829	1887	1974	2040	•	
TTTTTGTATTTTAG			2145 2146 2160	CCCAAAGTGCTGGGA	CCCAAAGTGCTGGGA	CCCAAAGTGCTGGGA	CCCAAAGTGCTGGGA		·
ACCACACCCAGTTAA	ACCACACCCAGTTAA		2130 2131 2145	CGCCCGCCTCGGCCT	CGCCCGCCTCGGCCT	GECCECCTCGGCCT	CGCCCCCTCGGCCT		
TTACAGATGCCCGCC	TTACAGATGCCCGCC		2115 2116 2130	TGGTCTCAAGTGATC	TGGTCTCAAGTGATC	TGGTCTCAAGTGATC	TGGTCTCAAGTGATC		·
CCTGAGTAGGTGGGA	CCTGAGTAGGTGGGA		2100 2101 211	CTGGTCTTGAACTCC	CTGGTCTTGAACTCC	CTGGTCTTGAACTCC	CTGGTCTTGAACTCC		
CTCTCACCTCAGCCT	CTCTCACCTCAGCCT		2085 2086 2100	TCCATGTTGGCCAGG	TCCATGTTGGCCAGG	TCCATGTTGGCCAGG	TCCATGTTGGCCAGG		
LC3 CGGGCTCAAGCGAIT CTCTCACCTCAGCCT CCTGAGTAGGTGGGA TTACAGATGCCCGCC ACCACACCCAGTTAA TTTTTGTATTTTTAG	LC4 CGGGCTCAAGCGATT CTCTCACCTCAGCCT CCTGAGTAGGTGGGA TTACAGATGCCCGCC ACCACACCCAGTTAA TTTTTGTATTTTTAG	e Veri	2071 2085	NOC2 AAGAGATGGGGTTTC TCCATGTTGGCCAGG CTGGTCTTGAACTCC TGGTCTCAAGTGATC CGCCCGCCTCGGCCT CCCAAAGTGCTGGGA	NL1 AAGAGATGGGGTTTC ICCATGTTGGCCAGG CIGGICITGAACTCC IGGTCTCAAGTGATC CGCCCGCCTCGGCCT CCCAAAGTGCTGGGA	LC1 AAGAGATGGGGTTTC TCCATGTTGGCCAGG CTGGTCTTGAACTCC TGGTCTCAAGTGATC GGCCGGCCTCGGCCT CCCAAAGTGCTGGGA	LC2 AAGAGATGGGGGTTTC TCCATGTTGGCCAGG CTGGTCTTGAACTCC TGGTCTCAAGTGATC CGCCGCCTCGGCCT CCCAAAGTGCTGGGA		
1,03	LC4			NOC2	NL1	101	1,02		

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2094	2160		1919	1977	2064	2130	2184	2250
5 LC3 AAGAGATGGGGTTTC TCCATGTTGGCCAGG CTGGTCTTGAACTCC TGGTCTCAAGTGATC CGCCCGCCTCGGCCT CCCAAAGTGCTGGGA	6 LC4 AAGAGATGGGGTTTC TCCATGTTGGCCAGG CTGGTCTTGAACTCC TGGTCTCAAGTGATC CGCCCGCCTCGGCCT CCCAAAGTGCTGGGA	2161 2175 2176 2190 2191 2205 2206 2220 2221 2235 2236 2250	1 NOC2 TTACAGGTGTGAGGC ACCGCACCAATCCT ATTAGGTTTCTTTGA ATCCCTCATGGCCT GCCTGGTTTTTGCTC AGCCTGTCTTCAGCT	2 NL1 TTACAGGIGIAGCC ACCGCACCCAATCCT ATTAGGTTTCTTIGA ATCCCCTCAIGGCCT GCCTGGTTTTIGCTC AGCCTGTCTTCAGCT	3 LC1 TTACAGGIGIGAGCC ACCGCACCCAATCCT ATTAGGITTCTTIGA ATCCCCTCAIGGCCT GCCTGGTTTTTGCTC AGCCTGTCTTCAGCT	4 LC2 TTACAGGTGTGAGGC ACCGCACCCAATGCT ATTAGGTTTCTTTGA ATCCCCTCATGGCCT GCCTGGTTTTTGCTC AGCCTGTCTTCAGCT	S LC3 TTACAGGTGTGAGGC ACCGCACCCAATCCT ATTAGGTTTCTTTGA ATCCCTCATGGCCT GCCTGGTTTTTGCTC AGCCTGTCTTCAGCT 2184	LC4 TTACAGGTGTGAGCC ACCGCACCCAATCCT ATTAGGTTTCTTTGA ATCCCTCATGGCCT GCCTGGTTTTTGCTC AGCCTGTCTTCAGCT
ູເດ	· •		-	2	е	4	S	v

2340	c 2009·	c 2067	c 2154	32 220	3C 2274	2340	•
• • •	ACGTGGCTCC	ACGTGGCTCC	ACGTGGCTCC	ACGTGGCTCC	ACGTGGCTCC	Acerecerc	
2325 2326	AGCCA GGGC	AGCCA GGGC	AGCCA GGGC	AGCCA GGGC	AGCCA GGGC	AGCCA GGGC	•
2310 2311	GTGCATCCCC	STGCATCCCC	GTGCATCCCC	GTGCATCCCC	GTGCATCCCC	GTGCATCCCC	
2310	AGCGTTCAG	AGCGTTCAG (AGCGTTCAG (AGCGTTCAG	AGCGTTCAG	AGCGTTCAG	
2295 2296	3 AAGAGC	AAGAGC	, AAGAGC	. AAGAGC	, AAGAGC	, AAGAGC	
2280 2281 229	rgaacrcacrrgcre	TGAACTCACTTGCTG	rgaacrcacrrgcrg	TGAACTCACTTGCTG	TGAACTCACTTGCTG	TGAACTCACTTGCTG	•
2266	CTCTGGTGGATGCTA	CTCTGGTGGATGCTA	CTCTGGTGGATGCTA	CTCTGGTGGATGCTA	CTCTGGTGGATGCTA	CTCTGGTGGATGCTA	
2251 2265	1 NOC2 TGAGGAGCTGGGAAG CTCTGGTGGAAGCTA TGAACTCACTTGCTG AAGAGCAGCGTTCAG GTGCATCCCCAGCCA GGGCACGTGGCTCCC	2 NL1 TGAGGAGCTGGGAAG CTCTGGTGGATGCTA TGAACTCACTTGCTG AAGAGCAGCGTTCAG GTGCATCCCCAGCCA GGGCACGTGGCTCCC	3 LCI. TGAGGAGCTGGGAAG CTCTGGTGGATGCTA TGAACTCACTTGCTG AAGAGCAGCGTTCAG GTGCATCCCCAGCCA GGGCACGTGGCTCCC	LC2 TGAGGAGCTGGGAAG CTCTGGTGGATGCTA TGAACTCACTTGCTG AAGAGCAGCGTTCAG GTGCATCCCCAGCCA GGGCACGTGGCTCCC	5 LC3 TGAGGAGCTGGGAAG CTCTGGTGGAATGCTA TGAACTCACTTGCTG AAGAGCAGCGTTCAG GTGCATCCCCAGCCA GGGCACGTGGCTCCC	6 LC4 TGAGGAGCTGGGAAG CTCTGGTGGATGCTA TGAACTCACTTGCTG AAGAGCAGCGTTCAG GTGCATCCCCAGCCA GGGCACGTGGCTCCC	
	1 NOC2	2 NL1	3 LC1	4 LC2	5 LC3 '	6 LC4	

1 NOC2 TGGAAGGGCCTTCTC TCCAAGCTGGGAGCT CCTGGGCCCCCACCA TTCACTTTTGTCCT TGCTGCTGGCAAACA GTAAAGAAACTCACT 2279 2 NL1 TGGAAGGCCTTCTC TCCAAGCTGGGAGCT CCTGGGCCCCCACCA TTCACTTTTTGTCCT TGCTGCTGGCAAACA GTAAAGAAACTCACT 2337

2 NLI TCAGCCATGAATTCA CTTCTCTTCAGGAGG TTTGGCTTGGC			4 LC2 TCAGCCATGAATTCA CTTCTCTTCAGGAGG TTTGGCTTGGC	5 LC3 TCAGCCATGAATTCA CTTCTCTTCAGGAGG TTTGGCTTGGC	6 LC4 TCAGCCATGAATTCA CTTCTCTTCAGGAGG TTTGGCTTGGC	2445 2446 2460 2461 2475 2476 2490 2491 2505 2506 2520	1 NOC2 CCCTGAAGAGAGA ACGTGTGTGTGTGT TCGGTGATCACCC TCCCATCCTTCCTGC CTCCTGCCCCAAACC CCGGGTTCCTGGGTC 2189	2 NL1 CCCTGAAGAGAGAGA ACGTGTGTGTGTGTGT TCGGTGATCACCC TCCCATCCTTCCTGC CTCCTGCCCCAAACC CCGGGTTCCTGGGTC 2247	3 LC1 CCCTGAAGAGAGAGA ACGTGTGTGTGTGTG TCGGTGATCACACCC TCCCATCCTTCCTGC CTCCTGCCCCAAACC CCGGGTTCCTGGGTC 2334	4 LC2 CCTGAAGAGAGAGA AGGTGTGTGTGTGT TCGGTGATCACACCC TCCCATCCTTCCTGC CTCCTGCCCCAAACC CCGGGTTCCTGGGTC 2400	5 LC3 CCCTGAAGAGAGA ACGTGTGTGTGTGTG TCGGTGATCACACCC TCCCATCCTTCCTGC CTCCTGCCCCAAACC CCGGGTTCCTGGGTC 2454	6 LC4 CCCTGAAGAGAGAGA ACGTGTGTGTGTGT TCGGTGATCACACCC TCCCATCCTTCCTGC CTCCTGCCCCAAACC CCGGGTTCCTGGGTC 2520	2535 2536 2550 2551 2565 2566 2580 2581 2595 2596 2610
	A CTTCTCT	A CTTCTCTI	A CTTCTCT1	· crrcrcrr	CTTCTCTT	5 2446	A ACGTGTGT	ACGTGTGT	ACGTGTGT	ACGIGIG	ACGIGIG	ACGTGTGT	5 2536
TCAGCCATGAATTC		TCAGCCATGAATTC	TCAGCCATGAATTC	TCAGCCATGAATTCA	TCAGCCATGAATTCA	2431 244	CCCTGAAGAGAGAG	CCCTGAAGAGAGAGA	CCCTGAAGAGAGAGA	CCCTGAAGAGAGA	CCCTGAAGAGAGAGA	CCCTGAAGAGAGAGA	2521 2538
1 NOCZ TCAGCCATGAA	2 NL1	3 LC1	4 · LC2	5 LC3	6 LC4		1 NOC2	2 NL1	3 LC1	4 LC2	5 LC3	6 LC4	. :

2424	2490	2544	2610	٠.							
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TGCTGCTGGCAAACA (TGCTGCTGGCAAACA (TGCTGCTGGCAAACA (TGCTGCTGGCAAACA (
TTTTGTCCT	TTTTGTCCT	TTTTGTCCT	TTTTGTCCT	•		2327	2385	2472	2538	2592	2658
TTCACT	TTCACT	TTCACT	TTCACT	•	2655 2656				. •		AAA
CTGGGCCCCCACCA	CTGGGCCCCCACCA	CTGGGCCCCCACCA	CTGGGCCCCCACCA			AAACAATGAAGATTA	AAACAATGAAGATTA	AAACAATGAAGATTA	AAACAATGAAGATTA	AAACAATGAAGATTA	AAACAATGAAGATTA
 CAAGCTGGGAGCT C	CAAGCTGGGAGCT C	CCAAGCTGGGAGCT	CCAAGCTGGGAGCT C		1626 2640 2641	ATGCTTCAGAATTA A	ATGCTTCAGAATTA A	ATGCTTCAGAATTA P	ATGCTTCAGAATTA P	ATGCTTCAGAATTA A	ATGCTTCAGAATTA A
3 LC1 TGGAAGGGCCTTCTC TCCAAGCTGGAAGCT CCTGGGCCCCCACCA TTCACTTTTTGTCCT TGCTGGTGAAACA GTAAAGAAACTCACT	4 LC2 TGGAAGGGCCTTCTC TCCAAGCTGGGAGCT CÇTGGGCCCCCACCA ITCACTTTTTGTCCT TGCTGGTGAAACA GTAAAGAAACTCACT	5 LC3 TGGAAGGGCCTTCTC TCCAAGCTGGAGCT CCTGGGCCCCCACCA TTCACTTTTTGTCCT TGCTGGTGGCAAACA GTAAAGAAACTCACT	6 LC4 TGGAAGGGCCTTCTG TCCAAGCTGGGAGCT CCTGGGCCCCCACCA TICACTTTTTGTCCT TGCTGGCAAACA GTAAAGAAACTCACT		2611 2625 2626	1 NOC2 TTCCCTGTGGCACGT TATGCTTCAGAATTA AAACAATGAAGATTA AAA	2 NL1 TICCCIGIGGCACGI TAIGCITCAGAAITA AAACAAIGAAGAITA AAA	TTCCCTGTGGCACGT TATGCTTCAGAATTA AAACAATGAAGATTA AAA			
3 LC1 1	4 LC2 1	5 LC3 T	6 LC4 1	£	.,	1 NOC2	2 NL1 1	3 LC1 1	4 LC2 1	5 LC3	6 LC4

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	1	15 16 3	30 31	45 46 6	60 61 7	75 76 90	÷
NOC	MADTIFGSGNDQW	1 NOC2 MADTIFGSGNDQWVC PNDRQLALRAKLQTG WSVHTYQTEKQRRKQ HLSPAEVEAILQVIQ RAERLDVLEQQRIGR LVERLETMRRNVMGN	3 WSVHTYQTEKORRK	Q HLSPAEVEAILQVIC) RAERLDVLEQQRIG	LVERLETMRRNVMGN	90
NL1	NL1 MADTIFGSGNDOWVC	/C PNDRQLALRAKLQTG	B WSVHTYQTEKQRRK(HLSPAEVEALLQVIQ	RAERLDVLEQQRIGR	PNDRQLALRAKLQTG WSVHTYQTEKQRRKQ HLSPAEVEALLQVIQ RAERLDVLEQQRIGR LVERLETMRRNVMGN	. 6
101	3 LC1 MADTIFGSGNDQWVC	/C PNDRQLALRAKLQTG	B WSVHTYQTEKQRRK(2 HLSPAEVÉAILOVIQ	RAERLDVLEQQRIGR	PNDRQLALRAKLQTG WSVHTYQTEKQRRKQ HLSPAEVÉAILQVIQ RAERLDVLEQQRIGR LVERLETMRRNVMGN	06
4 LC2						MRRNVMGN	©
1.03	5 LC3 MADTIFGSGNDQWVC	C PNDRQLALRAKLQTG	WSVHTYQTEKQRRKQ	PNDRQLALRAKLQTG WSVHTYQTEKQRRKQ HLSPAEVEALLQVIQ RAERLDVLEQQRIGR LVERLETMRRNVMGN	RAERLDVLEQQRIGR	LVERLETMRRNVMGN	06
6 LC4		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	MRRNVMGN	∞
			• .				
	91 10	105 106 120	120 121. 13	135 136 150	150 151 165	5 166 180	
NOC2	GLSQCLLCGEVLGE	1 NOC2 GLSQCLLCGEVLGFL GSSSVFCKDCRKKVC TKCGIEASPGQKRPL WLCKICSEQREVWKR SGAWFYKGLPKYILP LKTPGRADDPHFRPL	TKCGIEASPGQKRPI	. WLCKICSEQREVWKR	SGAWFYKGLPKYILP	LKTPGRADDPHFRPL	180
NL1	GLSQCLLCGEVLGF	2 NL1 GLSQCLLCGEVLGFL GSSSVFCKDCRK		VWKR	SGAWFYKGLPKYILP	VWKR SGAWFYKGLPKYILP LKTPGRADEPQFRPW	151
rcı	GLSQCLLCGEVLGF	3 LC1 GLSQCLLCGEVLGFL GSSSVFCKDCRKKVC TKCGIEASPGQKRPL WLCKICSEQREVWKR SGAWFYKGLPKYILP LKTPGRADDPHFRPL	TKCGIEASPGQKRPI	WLCKICSEQREVWKR	SGAWFYKGLPKYILP	LKTPGRADDPHFRPL	180
LC2	GLSQCLLCGEVLGF	4 LC2 GLSQCLLCGEVLGFL GSSSVFCKDCRKKVC TKCGIEASPGQKRPL WLCKICSEQREVWKR SGAWFYKGLPKYILP LKTPGRADDPHFRPL	TKCGIEASPGQKRPI	, WLCKICSEQREVWKR	SGAWFYKGLPKYILP	LKTPGRADDPHERPL	86
1,03	5 LC3 GLSQCLLCGEVLĢFL	1 GSSSVFCKDCRKKVC	TKCGIEASPGOKRPI	. WLCKICSEQREVWKR	SGAWFYKGLPKYILP	GSSSVFCKDCRKKVC TKCGIEASPGQKRPL WLCKICSEQREVWKR SGAWFYKGLPKYILP LKTPGRADDPHFRPL	180
LC4	GLSQCLLCGEVLGF	6 LC4 GLSQCLLCGEVLGFL GSSSVFCKDCRKKVC TKCGIEASPGQKRPL WLCKICSEQREVWKR SGAWFYKGLPKYILP LKTPGRADDPHFRPL	TKCGIEASPGOKRPI	, WLCKICSEQREVWKR	SGAWFYKGLPKYILP	LKTPGRADDPHFRPL	86

•		270	241	270	210	128	188									
	256 270	PGHLSGCQSSLASG	ESGGSVEAPRMGFTQ PAGHLFGLQSSLASG	ESGGSVEAPRMGFTQ PAGHLFGLQSSLASG			AGHLFGLQSSLASG									
4	255 2	SVEAPRMGFTH P	SVEAPRMGFTO PA	SVEAPRMGFTQ PA			SVEAPRMGFTQ P									
	240 241	SDKPWK ESGG	DKPWK ESGG	DKPWK ESGG	1		OKPWK ESGG		330	3 315	3 296	325	243	210	. 128	-
	225 226	PSTGVRDRKG	PSTGVRDRKGDKPWK	PSTGVRDRKGDKPWK	1		PSTGVRDRKG		316	APAGPSSCLG	APAGPSSCLG	APAGPSSCLG	APAGPSSCLG		!	
		DSDLSSSSLEDRL	SDLSSSSLEDRL	SDLSSSSLEDRL		* * * * * * * * * * * * * * * * * * * *	OSDLSSSSLEDRL	la .	315	PREGLIRR APVKDTFGRAFAADA APAGPSSCLG	VKDTPGRAPADA	VKDTPGRAPAADA	VKDTPGRAPADA	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	•
	5 210 211	RIYTWARGRVVSSDS DSDSDLSSSSLEDRL PSTGVRDRKGDKPWK ESGGSVEAPRWGFTH PPGHLSGCQSSLASG	PTEPAEREPRSSETS RIYTWARGRVVSSDS DSDSDLSSSSLEDRL	RIYTWARGRVVSSDS DSDSDLSSSSLEDRL	RIYTWARGRVVGRKC	TWARGRVVGRKC	RIYTWARGRVVSSDS DSDSDLSSSSLEDRL PSTGVRDRKGDKPWK ESGGSVEAPRMGFTQ PAGHLFGLQSSLASG		5 300 301	PRPGLTRR AE	SADPPGGPRPGLTRR APVKDTPGRAPAADA APAGPSSCLG	SADPPGGPRPGLTRR APVKDTPGRAPAADA APAGPSSCLG	SADPPGGPRPGLIRR APVKDIPGRAPAADA APAGPSSCLG		. 1	
	195 196	AEREPRSSETS RIY	EREPRSSETS RIY	PTEPAEREPRSSETS RIY	PTEPAEREPRSSETS RIY	5 LC4 PTEPAEREPRSSETS RIYTWARGRVVGRKC	AEREPRSSETS RIY		285 286	GSADPPGG	ETGTGSADPPGGGTG SAL		SSADPPGGGTG SAL			
	181	1 NOC2 PTEPAEREPRSSETS	2 NL1 PTEPA	3 LC1 PTEPA	4 LC3 PTEPA	5 LC4 PTEPA	6 LC2 PTEPAEREPRSSETS	•	271	1 NOC2 ETGTGSADPPGG-	2 NL1 ETGTO	3 LC1 ETGTGSADPPGGGTG	4 LC2 ETGTGSADPPGGGTG	5 LC3	6 LC4	
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